```
NL/4/01  (B   AACAGACAGA CCACCCAAAC AACCGCAGAG AAAAAGCCAA CCAGAGCAAC AACCAAAA--
UK/5/01  (B   AACAGACAGA CCACCCAAAC AACTGCAGAG AAAAAGCCAA CCAGAGCAAC AACCAAAA--

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
NL/1/00  (p   ---------- -AACACATTC TCCACCACGG GCAACGACAA GGACGGC--A CGCAG-AACC
BR/2/01  (A   ---------- -AACACATTC TCCACCACGG GCAACGACAA GGACGGC--A CGCAGGAACC
FL/4/01  (A   ---------- -AACACACTC TCCACCATGG GCAACGACAA GGACGGC--A CGCAG-AACC
FL/3/01  (A   ---------- -AACACATTC TCCACCATGG GCAACGACAA GGACGGC--A CGCAG-AACC
FL/8/01  (A   ---------- -AACACATTC TCCACCATGG GCAACGACAA GGACGGC--A CGCAG-AACC
FL/10/01 (    ----.----- -AACACATTC CCCACCATGG GCAATGACAA GGACGGT--C CGCGG-AACC
NL/10/01 (    ---------- -AACACATTC CCCACCATGG GCAATGACAA GGACGGT--C CGTGG-AACC
NL/2/02  (A   ---------- -AACACATTC CCCACCATGG GCAATGACAA GGACGGT--C CGTGG-AACC
NL/17/00 (    ---------- -TACACAATC ACCACCACGG ACAACAACGA AGGCAAT--C CGCAG-AGCC
NL/1/81  (A   ---------- -AACACAATC CCCACTACGG GCAACAACGA AGGCGGT--C CTCAG-AGCC
NL/1/93  (A   ---------- -AACACAATC ACCACCACGG GCAACAACGA AGGCGGT--C CTCAG-AGAC
NL/2/93  (A   ---------- -AACACAATC ACCACCACGG GCAACAACGA AGGCGGT--C CTCAG-AGCC
NL/3/93  (A   ---------- -AACACAATC CTCAATACGG GCAACAACGA AGGCGGT--C CTCAG-AGAC
NL/1/95  (A   ---------- -AACACAATC CCCACTACGG GCAACAACGA AGGCGGT--C CTCAG-AGCC
NL/2/96  (A   ---------- -CACACAATC CCCACCACGG GTAACAACGA AGGCGGT--C CTCAG-AGCC
NL/3/96  (A   ---------- -AACACAATC CCCACTACGG GCAACAACGA AGGCGGT--C CTCAG-AGCC
NL/22/01 (    ---------- -AACACAGTC CCCACCACGG ACAACACCGA AGGCGGT--C CCCAG-AGCC
NL/24/01 (    ---------- -AACACAGTC CCCACCACGG ACAACAACGA AGGCGGT--C CCCAG-AGCC
NL/23/01 (    ---------- -AACCACAGTC CCCACTACGG ACAACAGCGA AGGCGGT--C CCCAG-AGCC
NL/29/01 (    ---------- -TACACAATC CCCACCACGG GCAACAACGA AGGCAAT--C CGCAG-AGCC
NL/3/02  (A   ---------- -TACACAATC CCCACCACGG GCAACAACGA AGGCAAT--C CGCAG-AGCC
NL/1/99  (p   AGGGAAAAAG GAAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCAAC CCAAACAACC
NL/11/00 (    AGGGAAAAAG AAAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCAAC CCAAACAACC
NL/12/00 (    AGGGAAAAAG GGAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCTAC CCAAACAACC
NL/5/01  (B   AGGGAAAAAG GAAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCAAC CCAAACAACC
NL/9/01  (B   AGGGAAAAAG GAAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCAAC CCAAACAACC
NL/21/01 (    AGGGAAAAAG GAAAAGAAAA CACAAACCAA ACCACAAGCA CAGCTGCAAC CCAAACAACC
NL/1/94  (p   ---------- ---AAGAAAC CACAACTCGA ACTACAAGCA CAGCTGCAAC CCAAACACTC
NL/1/82  (B   ---------- ---AAGAAAC CACAACTCGA ACCACAAGCA CAGCTGCAAC CCAAACATTC
NL/1/96  (B   ---------- ---AAGAAAC CACAACTCGA ACCACAAGCA CAGCTGCAAC CCAAACACTC
NL/6/97  (B   ---------- ---AAGAAAC CACAACCCGA ACTACAAGTA CAGCTGCAAC CCAAACACCC
NL/9/00  (B   ---------- ---AAGAAAC CACAACTCGA ACCACAAGCA CAGCTGCAAC CCAAACACTC
NL/3/01  (B   ---------- ---AAGAAAC CATAACTCGA ACCACAAGCA CAGCCGCAAC CCAAACACTC
NL/4/01  (B   ---------- ---AAGAAAC CATAACTCGA ACCACAAGCA CAGCTGCAAC CCAAACACTC
UK/5/01  (B   ---------- ---AAGAAAC CACAACTCGA ACCACAAGCA CAGCTGCAAC CCAAACACTC

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   545        555        565        575        585        595
NL/1/00  (p   ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACCGTCCA CAGCATCAGT CCAACCTGAC
BR/2/01  (A   ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACCGTCCA CAGCATCAGT CCAACCTGAC
FL/4/01  (A   ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACCGTCCA CAGCATCAGT CCAACCCGAC
FL/3/01  (A   ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACCGTCCA CAGCATCAGT CCAACCCGAC
FL/8/01  (A   ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACCGTCCA CAGCATCAGT CCAACCCGAC
FL/10/01 (    ACCACTCTCC GCACAAGCAG CACAAGAAAG AGACTATCTA CAGCATCAGT CCAACCTGAC
NL/10/01 (    ACCACTCTCC GCACAAGCAG CATAAGAAAA AGACCGTCCA CAGCATCAGT CCAACCTGAC
NL/2/02  (A   ACCACTCTCC GCACAAGCAG CATAAGAAAA AGACCGTCCA CAGCATCAGT CCAACCTGAC
NL/17/00 (    ACCACTTTCC GCATGAGCAG CACAGGAAAA AGACCAACCA CAACATTAGT CCAGTCCGAC
NL/1/81  (A   ACCGCTTTCC GCACGAGCAG CACAGGAAAA AGACCAACCA CAACATCAGT CCAGTCTGAC
NL/1/93  (A   ACCGCCTTCC ACACGAGCAG CACAGGAAAA AGACCAACCA CAACATCAGT CCAGTCTGGC
NL/2/93  (A   ACCGCCTTCC ACACGAGCAG CACAGGAAAA AGACCAACCA CAACATCAGT CCAGTCTGGC
NL/3/93  (A   ACCGCCTTTC GCACGAGCAG CACAGGAGAG GGACCAACCA CAACATCGGT CCAGTCTGAC
NL/1/95  (A   ACCGCCTTTC GCACGAGCAG CACAGGAGAG GGACCAACCA CAACATCGGT CCAGTCTGAC
NL/2/96  (A   ACCGTCTTCC GCATGAGCAG CACAGGAAAA AGACCAACCA CAACATTAGT CCAGTCCGAC
NL/3/96  (A   ACCGCCTTTC GCATGAGCAG CACAGGAGAG GGACCAACCA CAACATCGGT CCAGTCTGAC
NL/22/01 (    ACCGCCCTTC GCACGAGCAG CACAGGAGAA AGACCAACCA CAACACCAGT CCAGCCCGAT
NL/24/01 (    ACCGCCCTTC GCACGAGCAG CACAGGAGAA AGACCAACCA CAACACCAGT CCAGCCCGAT
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NL/23/01 (.  ACCGCCCTTC GCACGAGCAG CACAGGAGAA AGACCAACCA CAACACCAGT CCAGCCCGAT
NL/29/01 (   ACCACCCTCC GCATGAGCAG CACAGGAAGA AGACCAACCA CAACACTAGT CCAGTCCGAC
NL/3/02 (A   ACCACCCTCC GCATGAGCAG CACAGGAAGA AGACCAACCA CAACACTAGT CCAGTCCGAC
NL/1/99 (p   AACACCACCA ACCAAATCAG AAATGCAAGT GAGACAATCA CAACATCCGA CAGACCCAGA
NL/11/00 (   AACACCACCA ACCAAACCAG AAATGCAAGT GAGACAATCA CAACATCCGA CAGACCCAGA
NL/12/00 (   AACACCACCA ACCAAATCAG AAATGCAAGC GAGACAATCA CAACATCCGA CAGACCCAGA
NL/5/01 (B   AACACCACCA ACCAAATCAG AAATGCAAGC GAGACAATCA CAACATCCGA CAGACCCAGA
NL/9/01 (B   AACACCACCA ACCAAATCAG AAATGCAAGC GAGACAATCA CAACATCCGA CAGACCCAGA
NL/21/01 (   AACACCACCA ACCAAATCAG AAATGCAATT GAGACAATCA CAACATCCGA CAGACCCAGA
NL/1/94 (p   AACACTACCA ACCAAACTAG CTATGTGAGA GAGGCAACCA CAACTCCGC CAGATCCAGA
NL/1/82 (B   AACACCACCA ATCAAACCAG AAATGGAAGA GAGACAACCA TAACATCTGC CAGATCCAGA
NL/1/96 (B   AACACCACCA ACCAAACTAG CAATGGAAGA GAGGCAACCA CAACATCCAC CAGATCCAGA
NL/6/97 (B   AACACCACCA ACCAAACCAG CAATGGAAGA GAGGCAACCA CAACATCTGC CAGGTCCAGA
NL/9/00 (B   AACACCACCA ACCAAACTAG CAATGGAAGA GAGGCAACCA CAACATCTGC CAGATCCAGA
NL/3/01 (B   AACACCACCA ACCAAACCAA CAATGGAAGA GAGGCAACCA CAACATCTGC CAGATCCAGA
NL/4/01 (B   AACACCACCA ACCAAACTAG CAATGGAAGA GAGGCAACCA CAACATCTGC CAGATCCAGA
UK/5/01 (B   AACACCACCA ACCAAACTAG CAATGGAAGA GAGGCAACCA CAACATCTGC CAGATCCAGA


            ...|....| ...|....| ...|....| ...|....| ...|....| ...|....|
               605       615       625       635       645       655
NL/1/00 (p   ATCAGCGCAA CAACCCACAA AAACGAAGAA GCAAGTCCAG CGAGCCCACA AACATCTGCA
BR/2/01 (A   ATCAGCGCAA CAACCCACAA AAACGAAGAA GCAAGTCCAG CGAGCCCACA AACATCTGCA
FL/4/01 (A   ATCAGCGCAA CAACCCACAA AAACGAAGAA GCAAGTCCAG CGAGCCCACA AACATCTGCA
FL/3/01 (A   ATCAGCGCAA CAACCCACAA AAACGAAGAA GCAAGTCCAG CGAGCCCACA AACATCTGCA
FL/8/01 (A   ATCAGCGCAA CAACCCACAA AAACGAAGAA GCAAGTCCAG CGAGCCCACA AACATCTGCA
FL/10/01 (   AGCAGCGCAA CAACCCACAA ACACGAAGAA ACAAGCCCAG TGAGCCCACA AACATCCGCA
NL/10/01 (   AGCAGCGCAA CAACCCACAA ACACGAAGAA GCAAGCCCAG TGAGCCCGCA AGCATCTGCA
NL/2/02 (A   AGCAGCGCAA CAACCCACAA ACACGAAGAA GCAAGCCCAG TGAGCCCGCA AGCATCTGCA
NL/17/00 (   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGTTCAG CGAACCCACA GGCGTCTGCA
NL/1/81 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAAGTTCAG CGAACCCACA GGCATCTGCA
NL/1/93 (A   AGCAGCACCA CAACTCAAAA TCATGAAGAA ACAAGTTCAT CGAACCCACA GGCATCTGCA
NL/2/93 (A   AGCAGCACCA CAACTCAAAA TCATGAAGAA ACAAGTTCAT CGAACCCACA GGCATCTGCA
NL/3/93 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGTTCAG CGAACCCACA GGCATCTGCA
NL/5/95 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGTTCAG CAAACCCACA GGCATCTGCA
NL/2/96 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGTTCAG CAAACTCACA GGCATCTGCA
NL/3/96 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCTGCA
NL/22/01 (   AGCAGCACCA CAACACAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCCGCA
NL/24/01 (   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCCGCA
NL/23/01 (   AGCAGCACCA CAACACAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCCGCA
NL/29/01 (   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCCGCA
NL/3/02 (A   AGCAGCACCA CAACCCAAAA TCATGAAGAA ACAGGCTCAG CGAACCCACA GGCATCTGCA
NL/1/99 (p   ACTGACACCA CAACCCAAAG CAGCGAACAG ACAA-CCCGG GCAACAGACC CAAGCTCCCC
NL/11/00 (   ATTGACACCA CAACCCAAAG CAGCGATCAG ACAA-CCCGG GCAACAGACC CAAGCTCCCC
NL/12/00 (   ACTGACTCCA CAACCCAAAG CAGCGAACAG ACAA-CCCGG GCAACAGACC CAAGCTCCCC
NL/5/01 (B   ACTGACTCCA CAACCCAAAG CAGCGAACAG ACAA-CCCAG GCAACAGACC CAAGCTCCCC
NL/9/01 (B   ACTGACTCCA CAACCCAAAG CAGCGAACAG ACAA-CCCGG GCAACAGACC CAAGCTCCCA
NL/21/01 (   ACTGACTCCA CAACCCAAAG CAGCGAACAG ACAA-CCCGG GCAACAGACC CAAGCTCCCA
NL/1/94 (p   AACGACGCCA CAACTCAAAG CAGCGAACAA ACAA-CCCGA GCAGCAGACC CAAGCTCCCA
NL/1/82 (B   AACGACGCCA CAACTCAAAG CAGCGAACAA ACAA-ACCAG ACAGCAGACC CAAGCTCCCA
NL/1/96 (B   AACGGTGCCA CAACTCAAAA CAGCGATCAA ACAA-CCTAG ACAGCAGACC CAAGCTCCCA
NL/6/97 (B   AACGGTGCCA CAACTCAAAG CAGCGATCAA ATAA-CCCAG GCAGCAGACT CAAGCTCCCA
NL/9/00 (B   AACAATGCCA CAACTCAAAG CAGCGACCAA ACAA-CCCAG GCAGCAGAAC CAAGCTCCCA
NL/3/01 (B   AACAATGCCA CAACTCAAAG CAGCGACCAA ACAA-CCCAG GCAGCAGACC CAAGCTCCCA
NL/4/01 (B   AACAATGCCA CAACTCAAAG CAGCGACCAA ACAA-CCCAG GCAGCAGACC CAAGCTCCCA
UK/5/01 (B   AACAATGCCA CAACTCAAAG CAGCGATCAA ACAA-CCCAA GCAGCAGAAC CAAACTCCCA


            ...|....| ...|....| ...|....| ...|....| ...|....| ...|....|
               665       675       685       695       705       715
NL/1/00 (p   AGCACAACAA GAATACAAAG GAAAAGCGTG GAGGCCAACA CATCAACAAC ATACAACCAA
BR/2/01 (A   AGCACAACAA GAATACAAAG GAAAAGCGTG GAGGCCAACA CATCAACAAC ATACAACCAA
FL/4/01 (A   AGCACAACAA GAACACAAAG GAAAAGCGTG GAGGCCAACA CATCAACAAC ATACAACCAA
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FL/3/01  (A .  AGCACAACAA GAACACAAAG GAAAAGCGTG GAGGCCAACA CATCAACAAC ATACAACCAA
FL/8/01  (A     AGCACAACAA GAACACAAAG GAAAAGCGTG GAGGCCAACA CATCAACAAC ATACAACCAA
FL/10/01 (A     AGCACAGCAA GACCACAAAG GAAGGGCATG GAGGCCAGCA CATCAACAAC ATACAACCAA
NL/10/01 (      AGCACAGCAA GACCACAAAG GAAGGGCATG GAGGCCAGCA CATCAACAAC ATACAACCAA
NL/2/02  (A     AGCACAGCAA GACCACAAAG GAAGGGCATG GAGGCCAGCA CATCAACAAC ATACAACCAA
NL/17/00 (      AGCACAATG- -----CAAAA ---------- ---CTAGCA CACCAATAAT ATAAAACCAA
NL/1/81  (A     AGCACAATG- -----CAAAG ---------- ---CCAGCA CACCAACATA ATAAAACCAA
NL/1/93  (A     AGCACAATG- -----CAAGA ---------- ----CCAGA CACCAACAAT ACAAAACAAA
NL/2/93  (A     AGCACAATG- -----CAAGA ---------- ----CCAGA CACCAACAAT ACAAAACAAA
NL/3/93  (A     AGCACAATG- -----CAAAA ---------- ---CTAGCA CACCAACATT GTAAAACCAA
NL/1/95  (A     AGCACAATG- -----CAAAA ---------- ---CTAGCA CACCAACATT GTAAAACCAA
NL/2/96  (A     AGCACAATG- -----CAAAA ---------- ---CTAGCA CTCCAACAAT ATAAAACCAA
NL/3/96  (A     AGCACAATG- -----CAAAA ---------- ---CCAGCA CACCAACATT GCAAAACCAA
NL/22/01 (A     AGCACAATG- -----CAAAA ---------- ----CCAGA CACCAACATT GCAAGACCAA
NL/24/01 (      AGCACAATG- -----CAAAA ---------- ----CCAGA CACCAACATT GCAAGACCAA
NL/23/01 (      AGCACAATG- -----CAAAA ---------- ----CCAGA CACCAACATT GCAAGACCAA
NL/29/01 (      AGCACAATG- -----CAAAA ---------- ----CCAGA CACCAACAAT ATAAAACCAA
NL/3/02  (A     AGCACAATG- -----CAAAA ---------- ---CCAGCA CACCAACAAT ATAAAACCAA
NL/1/99  (p     ACCACACCAT GCATAGAGAG GTGCA----- -AAACTCAAA TGAGCACAAC ACACAAACAT
NL/11/00 (      ACCACACCAT GCACAGAGTG GTGCA----- -AAACCCAAA TGAACACAAC ACACAAACAT
NL/12/00 (      ACCACATCAT GCACAGGGAA GTGCA----- -AAACCCAAA TGAACACAAC ACACAAACAT
NL/5/01  (B     AGCACACCAT GCACAGGGAA GTGCA----- -AAACCCAAA TGAACACAAC ACACAAACAT
NL/9/01  (B     ACCACACCAT GCACAGGGAA GTGCA----- -AAACCCAAA TGAACACAAC ACACAAACAT
NL/21/01 (      CCCACACCAT GCACAGGGAA GTGCA----- -AAACCCAAA TGAACACAAC ACACAAACAT
NL/1/94  (p     ACCACACCAT ACACAGAAAA GCACA----- -ACAACACAA T----ACAAC ACAGACACAT
NL/1/82  (B     ACCACATCAT GCATAGATAA GCACA----- -ATAACAATA TGAACACAAC ACAGACACAT
NL/1/96  (B     ACCACACCAT ACACAGAAAA GCACA----- -ACAACAACA T----ACAAC ACAGACACAT
NL/6/97  (B     ACCACACCAT ACACAGAAAA GCACA----- -ACAACAGCA T----ACAAC ACAGACACAT
NL/9/00  (B     ATCACAACAT ACACAGAAAA GCACA----- -ACAACAACA T----ACAAC ACAGACACAT
NL/3/01  (B     ATCACAACAT ACACAGAAAA GCATA----- -ACAACAACA T----ACAAC ACAGACACAT
NL/4/01  (B     ATCACAACAT ACACAGAAAA GCACA----- -ACAACAACA T----ACAAC ACAGACACAT
UK/5/01  (B     ATCACAACAT ACACAGAAAA GCACA----- -ACAACAACA T----ACAAC ACAGACACAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   725        735        745        755        765        775
NL/1/00  (p     ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGCAGACAC CAACAATGGA
BR/2/01  (A     ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGCAGACAC CAACAATGGA
FL/4/01  (A     ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGCAGACAC CAACAATGGA
FL/3/01  (A     ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGCAGACAC CAACAATGGA
FL/8/01  (A     ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGCAGACAC CAACAATGGA
FL/10/01 (      ACTAGTTAAC AAAAAATACA AAATAACTCT AAGATAAACC ATGTAGACAC CAACAATTGA
NL/10/01 (      ACTAGTTAAC AAAAAATATA AAATAACTCT AAGATAAACC ATGTAGACAC CAACAATTGA
NL/2/02  (A     ACTAGTTAAC AAAAAATATA CAATAACTCT AAGATAAACC ATGTAGACAC CAACAATTGA
NL/17/00 (      ATTAGTTAAC AAAAAATGCG AGATAGCTCT AAAGCAAACA ATGTAGGTAC CAACATCAA
NL/1/81  (A     ATTAGTTAAC AAAAAATACG AGATAGCTCT AAAGTAAAAC ATGTAGGTAC CAACATCAA
NL/1/93  (A     ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTAC CAACAGTAAA
NL/2/93  (A     ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTAC CAACAGTAAA
NL/3/93  (A     ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTGC TAACAATCAA
NL/1/95  (A     ATTAGTTAAC AAAAAATATG AAATAGTTCT AAAGTAAAAC ATGTAGGTGC TAACAATCAA
NL/2/96  (A     ATTAGTTAAC AAAAAATACG AGATAGCTCT AAAGTAAAAC ATGTAGGCAC CAACAATCAG
NL/3/96  (A     ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTGC CAACATCAA
NL/22/01 (      ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTGC CAACATCAA
NL/24/01 (      ATTAGTTAAC AAAAAATATG AAATAGCTCT AAAGTAAAAC ATGTAGGTGC CAACATCAA
NL/23/01 (      ATTAGTTAAC AAAAAATACG AGATAGCTCT AAAGTAAAAC ATGTAGGTGC CAACATCAA
NL/29/01 (      ATTAGTTAAC AAAAAATACG AGATAGCTCT AAAGTAAAAC ATGTAGGCAC CAACATCAA
NL/3/02  (A     ATTAGTTAAC AAAAAATACG.AGATAGCTCT AAAGTAAAAC ATGTAGGCAC CAACAATCAA
NL/1/99  (p     CCCATCCAAG TAGTTA-ACA AAAAA-CCAC AAAATAA-CC TTGAAAAAC-C AAAAAA--CC
NL/11/00 (      CTCATCCAAG TAGTTA-ACA AAAAA-CCAC AAAATAA-CC TTGAAAAAC-C AAAAAA--CC
NL/12/00 (      CCCATCCAAG TAGTTA-ACA AAAAA----- ---------- ---------- ----------
NL/5/01  (B     CCCATCCAAG TAGTTA-ACA AAAAA-A--- ---------- ---------- ----------
NL/9/01  (B     CCCATCCAAG TAGTTA-ACA AAAAA----- ---------- ---------- ----------
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NL/21/01 (.  CCCATCCAAG TAGTTA-ACA AAAAA----- ---------- ---------- ----------
NL/1/94 (p   CCTCTCCAAG TAGTTA-ACA AAAAAACTAT AAAATAA-TC ATGAAAAC-C GAAAAA-CTA
NL/1/82 (B   CTTCTCCAAG TAGTTA-ACA AAAAA-CTAT AAAATAA-CC ATGAAAAC-C AAAAAA-CTA
NL/1/96 (B   CTTCTCCAAG TAGTTA-ACA AAAAA-CTAT AAAATAA-CC ATGAAAAC-T ATGAAAAC-T AAAAAA-CTA
NL/6/97 (B   CTTTTCCAAG TAGTTA-ACA AAAA-CTAT AAAATAA-CC ATGAAAAC-C ATGAAAAC-T AAAAAA-CTA
NL/9/00 (B   CTTCTCTAAG TAGTTA-ACA AAAAAACTAT AAAATAA-CC ATGAAAAC-C AAAAAA-CTA
NL/3/01 (B   CTTCTCCAAG TAGTTA-ACA AAAAAACTAT AAAATAA-CC ATGAAAAC-C AAAAAAACTA
NL/4/01 (B   CTTCTCCAAG TAGTTA-ACA AAAAAACTAT AAAATAA-CC ATGAAAAC-C AAAAAAACTA
UK/5/01 (B   CTTCTCTAAG TAGTTA-ACA AAAAAACTAT AAAATAA-CC ATGAAAAC-C AAAAAA-CTA
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                785        795        805        815        825        835
NL/1/00 (p   GAAGCCAAAA GACAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCTG
BR/2/01 (A   GAAGCCAAAA GACAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCTG
FL/4/01 (A   GAAGTCAAAA GACAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCTG
FL/3/01 (A   GAAGTCAAAA GACAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCTG
FL/8/01 (A   GAAGTCAAAA GACAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCTG
FL/10/01 (   GAAGCCAAAA GGCAATTCAC AATCTCCC-A AAAAAGCAAC AACACCATAT TAGC--TCCG
NL/10/01 (   GAAGCCAAAA GGCAATTCAC AATCTCCCCA AAAAGGCAAC AACACCATAT TAGC--TCCG
NL/2/02 (A   GAAGCCAAAA GGCAATTCAC AATCTCCC-A AAAAGGCAAC AACACCATAT TAGC--TCCG
NL/17/00 (   GAAACCAAAA GACAACTCAC AATCTCCCTA AAACAGCAAC GACACCATGT CAGC--TTTG
NL/1/81 (A   GGAATCAAAA GACAACTCAC AATCTCCCTA AAACAGCAAC AACATCATGT CAGT--TTTG
NL/1/93 (A   GAAATCAAAA GACAACTCAC AATCTCCCCA AAACAGCAAC AACATCATGT CAGC--TTCG
NL/2/93 (A   GAAATCAAAA GACAACTCAT AATCTCCCCA AAACAGCAAC AACATCATGT CAGC--TTCG
NL/3/93 (A   GAAATCAAAA GACATCTCAT AATCTTCTCA AAACAGCAAC AACATCATGT CAAC--TTTG
NL/1/95 (A   GAAATCAAAA GACAACTCAT AATCTCCCTA AAACAGCAAC AACATCATGT CAAC--TTTG
NL/2/96 (A   GAAATTAAAA GACAACTCAC AACCTCCCTA AAACAGCAAC GACACCATGT CAAC--TTTG
NL/3/96 (A   GAAATCAAAA GACAACTCAC AATCTCCCTA AAACAGCAAC AACATCATGC CAAC--TTTG
NL/22/01 (   GAAATCAAAA GATAACTCAT AATCTCTCTA AAACATCAAC AACATCATGT TAAC--TTTG
NL/24/01 (   GAAATCAAAA GATAACTCAT AATCTCTCTA AAACATCAAC AACATCATGT TAAC--TTTG
NL/23/01 (   GAAATCAAAA GATAACTCAC AATCTCTCTA AAACATCAAC AACATCATGT TAAC--TTTG
NL/29/01 (   GAAACCAAAA GATAACTCAC AATCCCCCCA AAACAGCAAC GACACCATGT CAGC--TTTG
NL/3/02 (A   GAAACCAAAA GATAACTCAC AATCCCCCCA AAACAGCAAC GACACCATGT CAGC--TTTG
NL/1/99 (p   A-----AAAC ATAAACCCAG A---CCCAGA AA--ACATA GACACTATAT GGAAGGTTCT
NL/11/00 (   A-----AACC ACAAACTTAG A---CCCAGA AA--AACATA GACACTATAT GGAAGGTTTG
NL/12/00 (   ---------- ------TCAG A---CCCAGA AA--CCCAGA AA--AACATA GACACTATAT GGAAGGTCCG
NL/5/01 (B   ---------- ------TCAG A---CCCAGA AA--AACACA GACACTATAT GGAAGGTCCG
NL/9/01 (B   ---------- ------TCAG A---CCCAGA AA--AACATA GACACTATAT GGAAGGTCCG
NL/21/01 (   ---------- ------TCAG A---CCCAGA AA--AACATA GACACTATAT GGAAGGTCCG
NL/1/94 (p   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTGTTTG
NL/1/82 (B   G-----AAAA GTAAATTTGA A---CTCAGA AAAGAACACA AACACTAAAT GAATTGTTTG
NL/1/96 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTGTTTG
NL/6/97 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTGTTTG
NL/9/00 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTATTTG
NL/3/01 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTGTTTG
NL/4/01 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAAGAACACA AACACTATAT GAATTGTTTG
UK/5/01 (B   G-----AAAA GTTAATTTGA A---CTCAGA AAGGAACACA AACACTATAT GAATTATTTG
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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                845        855        865        875        885        895
NL/1/00 (p   CCCAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA AAATACCACA ACCACCCCAA
BR/2/01 (A   CCCAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA AAATACCACA ACCACCCCAA
FL/4/01 (A   CCCAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA AAATACCACA ACCACCCCAA
FL/3/01 (A   CCCAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA AAATACCACA ACCACCCCAA
FL/8/01 (A   CCCAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA AAATACCACA ACCACCCCAA
FL/10/01 (   CTTAAATCTC CCTGAAAAA- AACACTCACC CATATACCAA CTATACCACA ACCATCCCAA
NL/10/01 (   CTTAAATCTC CCTGGAAAA- AACACTCGCC CATATACCAA CTATACCACA ACCATCCCAA
NL/2/02 (A   CTTAAGTCTC CCTGGAAAA- AACACTCGCC CATATACCAA CTATACCACA ACCATCCCAA
NL/17/00 (   CTCAAATCTC TCTGGGAGA- AACTTCTACC CACATACTAA CAACATCACA ACCATCTCAA
NL/1/81 (A   CTCAAATCTC CCTGGGAGA- AACTTTCGCC CACATACTAA CAACATCACA ACCATCTCAA
NL/1/93 (A   CTCAAATCTC CCTGGGAGA- AACTCTCGCC CACATACTAA CAACATCACA ACTATCTCAA
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NL/2/93  (A   CTCAAATCTC CCTGGGGAGA- AACTCTCGCC CACATACTAA CAACATCACA ACTATCTCAA
NL/3/93  (A   CTCAAATCTC CCTGGGAGA- ACTTTCGCC CCCATACTGA CAACATCACA ATCATCTCAA
NL/1/95  (A   CTCAAATCTC CCTGGGGAGA- AACTTTCGCC CCCATACTGA CAACATCACA ATCATCTCAA
NL/2/96  (A   CTCAAATCTC TCTGGGGAGA- AACTTTCGCC CACATACTAA CAACATCACA ATCATCTCAA
NL/3/96  (A   CTCAAATCTC CCTGGGGAGA- AACCCTCGCC CCCATACTGA CAACATCACA ATCATCTCAA
NL/22/01 (    CTCAAATCTC TCTGGGGAGA- AACCTTCGCC CCCATACTGG CAACATCACA ATCATCTCAA
NL/24/01 (    CTCAAATCTC TCTGGGGAGA- AACCTTCGCC CCCATACTGG CAACATCACA ATCATCTCAA
NL/23/01 (    CTCAAATCTC TCTGGGGAGA- AACCTTCGCC CCCATACTGG CAACATCACA ATCATCTCAA
NL/29/01 (    CTCAAATCTC TCTGGGGAGA- AACTTTTGCC CACATACTAA CAACATCACA ACCATCTCAA
NL/3/02  (A   CTCAAATCTC TCTGGGGAGA- AACTTTTGCC CACATACTAA CAACATCACA ACCATCTCAA
NL/1/99  (p   AGCATATGCA CCAATGAGAT GGCATCTGTT CATGTATCAA TAGCACCACC ATCAT-TCAA
NL/11/00 (    AGCATATGCA CCAATGAAAT GGTATCTGTT CATGTATCAA TAGCCGCCACC ATTAT-TTAA
NL/12/00 (    AGCATATGCA CCGATGAAAT GGCATTTGTT CATGTATCAA TAGCGGCCACC ATTAT-TTAA
NL/5/01  (B   AGCATATGCA CCGATGAAAT GGCATCTGTT CATGTATCAA TAGCACCACC ATTAT-TTAA
NL/9/01  (B   AGCATATGCA CCGATGAAAT GGCATCTGTT CATGTATCAA TAGCCGCCACC ATTAT-TTAA
NL/21/01 (    AGCATATGCA CCGATGAAAT GGCATCTGTT CATGTATCAA TAGCACCACC ATTAT-TTAA
NL/1/94  (p   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
NL/1/82  (B   AGCATATATA CTAATGAAAT AGCATCTGTT CATGCATCAA TAATACCATC ATTAC-TTAA
NL/1/96  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
NL/6/97  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
NL/9/00  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
NL/3/01  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
NL/4/01  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA
UK/5/01  (B   AGCGTATATA CTAATGAAAT AGCATCTGTT TGTGCATCAA TAATACCATC ATTAT-TTAA

              ....|....| ....|....| ....|....
                      905        915        925
NL/1/00  (p   GAAAAAAA-C TGGGCAAAAC AACACCCAA
BR/2/01  (A   GAAAAAAA-C TGGGCAAAAC AACACCCAA
FL/4/01  (A   GAAAAAAA-C TGGGCAAAAC AACACCCAA
FL/3/01  (A   GAAAAAAA-C TGGGCAAAAC AACACCCAA
FL/8/01  (A   GAAAAAAA-C TGGGCAAAAC AACACCCAA
FL/10/01 (    GAAAAAAGGC TGGGCAAAAC AACACCCAA
NL/10/01 (    GGAAAAAAGC TGGGTAAAAC AACACCCAA
NL/2/02  (A   GAAAAAAAGC TGGGCAAAAC AACACCCAA
NL/17/00 (    GAAAAGAAAC TGGGCAAAAC AGCATCCAA
NL/1/81  (A   GAAAAGAAAC TGGGCAAAAC AGCACCCAA
NL/1/93  (A   GAAAAGAAAC TGGGCAAAAA AACACTCAA
NL/2/93  (A   GAAAAGAAAC TGGGCAAAAC AACACTCAA
NL/3/93  (A   GAAAAGAAAC TGGGCAAAAC AGCACCAAA
NL/1/95  (A   GAAAAGAAAC TGGGCAAAAC AGCACCAAA
NL/2/96  (A   GAAAAGAAAC TGGGCAAAAC AGCATCCAA
NL/3/96  (A   GAAAAGAAAC TGGGCAAAAC AGCACCAAA
NL/22/01 (    GAAAAGAAAC TGGGCAAAAC AACACCAAA
NL/24/01 (    GAAAAGAAAC TGGGCAAAAC AACACCAAA
NL/23/01 (    GAAAAGAAAC TGGGCAAAAC AACACCCAA
NL/29/01 (    GAAAAGAAAC TGGGCAAAAC AGCATCCAA
NL/3/02  (A   GAAAAGAAAC TGGGCAAAAC AACATCCAA
NL/1/99  (p   GGAATAAGAA GAGGCAAAA- ---ATTTAA
NL/11/00 (    GGAATAAGAA GAGGCAAAA- ---ATTCAA
NL/12/00 (    GGAATAAGAA GAGGCAAAA- ---ATTCAA
NL/5/01  (B   GGAATAAGAA GAGGCAAAA- ---ATTCAA
NL/9/01  (B   GGAATAAGAA GAGGCAAGA- ---ATTCAA
NL/21/01 (    GGAATAAGAA GAGGCAAGA- ---ATTCAA
NL/1/94  (p   GAAATAAGAA GAAGCTAAA- ---ATTCAA
NL/1/82  (B   GAAATAAGAA GAAGCAAAA- ---ATTCAA
NL/1/96  (B   GAAATAAGAA GAAGCTAAA- ---ATTCAA
NL/6/97  (B   GAAATAAGAA GAAGCTAAA- ---ATTCAA
NL/9/00  (B   GAAATAAGAA GAAGCTAAA- ---ATTCAA
NL/3/01  (B   GAATTAAGAA GAAGCTAAA- ---ATTCAA
NL/4/01  (B   GAATTAAGAA GAAGCTAAA- ---ATTCAA
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UK/5/01 (B   GAAATAAGAA GAAGCTAAA- ---ATTCAA

Alignment: G Protein

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          ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               5         15        25        35        45        55
NL/1/00  (p   MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLVLIGITT LSIALNIYLI INYKMQKNTS
BR/2/01  (A   MEVKVENIRT IDMLKASVKN RVARSKCFKN ASLVLIGITT LSIALNIYLI INYKMQKNTS
FL/4/01  (A   MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLVLIGITT LSIALNIYLI INYKMQKNTS
FL/3/01  (A   MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLVLIGITT LSIALNIYLI INYKMQKNTS
FL/8/01  (A   MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLVLIGITT LSIALNIYLI INYKMQKNTS
FL/10/01 (    MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTMQENTS
NL/10/01 (    MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTMQENTS
NL/2/02  (A   MEVKVENIRT IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTMQENTS
NL/17/00 (    MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSTALNIYLI INYTIQKTTS
NL/1/81  (A   MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/1/93  (A   MEVKVENIRA VDMLKARVKN RVARSKCFKN ASLILVGITT LSIALNIYLI VNYTIQKTTS
NL/2/93  (A   MEVKVENIRA VDMLKARVKN RVARSKCFKN ASLILVGITT LSIALNIYLI VNYTIQKTTS
NL/3/93  (A   MEVKVENIRA IDMLKARMKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/1/95  (A   MEVKVENIRA IDMLGKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/2/96  (A   MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/3/96  (A   MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/22/01 (    MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/24/01 (    MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/23/01 (    MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/29/01 (    MEVKVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQQTTS
NL/3/02  (A   MEVRVENIRA IDMLKARVKN RVARSKCFKN ASLILIGITT LSIALNIYLI INYTIQKTTS
NL/1/99  (p   MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/11/00 (    MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/12/00 (    MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/5/01  (B   MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/9/01  (B   MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/21/01 (    MEVRVENIRA IDMFKAKIKN RIRSSRCYRN ATLILIGLTA LSMALNIFLI IDHATLRNMI
NL/1/94  (p   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYAMLKNMT
NL/1/82  (B   MEVRVENIRT IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYATFKNMT
NL/1/96  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYAMLKNMT
NL/6/97  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYATLKNMT
NL/9/00  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYATLKNMT
NL/3/01  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLSA LSMALNIFLI IDYAKSKNMT
NL/4/01  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLSA LSMALNIFLI IDYAKSKIMT
UK/5/01  (B   MEVRVENIRA IDMFKAKMKN RIRSSKCYRN ATLILIGLTA LSMALNIFLI IDYATLKNMT

          ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65        75        85        95       105       115
NL/1/00  (p   ESEHHTSSSP MESSRETPTV PTDNSDTNSS PQHPTQQSTE GSTLYFAASA SSPETEPTST
BR/2/01  (A   ESEHHTSSSP MESSRETPTV PTDNSDTNSS PQHPTQQSTE GSTLYFAASA SSPETEPTST
FL/4/01  (A   ESEHHTSSSP MESSRETPTV PTDNSDTNSS PQHPTQQSTE GSTLYFAASA SSPETEPTST
FL/3/01  (A   ESEHHTSSSP MESSRETPTV PTDNSDTNSS PQHPTQQSTE GSTLYFAASA NSPETEPTST
FL/8/01  (A   ESEHHTSSSP MESSRETPTV PTDNSDTNSS PQHPTQQSTE GSTLYFAASA SSPETEPTST
FL/10/01 (    ESEHHTSSSP MESSRETPTV PIDNSDTNPG SQYPTQQSTE DSTLHSAASA SSPETEPTST
NL/10/01 (    ESEHHTSSSP MESSRETPTV PMDNSDTNPG SQYPTQQSTE GSTLHFAASA SSPETEPTST
NL/2/02  (A   ESEHHTSSSP MESSRETPTV PMDNSDTNPG SQYPTQQSTE GSTLHFAASA SSPETEPTST
NL/17/00 (    ESEHHTSSPP TEPNKEASTI STDNPDINPS SQHPTQQSTE NPTLNPAASA SPSETEPAST
NL/1/81  (A   ESEHHTSSPP TESNKETSTI PIDNPDINPN SQHPTQQSTE SPTLNPAASV SPSETEPAST
NL/1/93  (A   ESEHHTSSSP TESNKGTSTI PTDNPDINPN SQHPTQQSTE SPTLNTAASV SPSETEPAST
NL/2/93  (A   ESEHHTSSSP TESNKETSTI PIDNPDINPN SQHPTQQSTE SPTLNAASV SPSETEPAST
NL/3/93  (A   ESEHHTSSPP TESNKETSTI PIDNPDINPN SQHPTQQSTE SLTLNPAASV SPSETEPAST
NL/1/95  (A   ESEHHTSSPP TESNKETSTI SIDNPDINPN SQHPTQQSTE SLTLSPTASV SPSETEPAST
NL/2/96  (A   ESEHHTSSPP TESNKEASTI SIDNPDINPN SQHPTQQSTE NPTLNPAASV SSSETEPAST
NL/3/96  (A   ESEHHTSSPP TESNKETSTI SIDNSDINPN SQHPTQQSTE SLTLSPTASV SPSETEPAST
NL/22/01 (    ESEHHTSSPP TESNKETSTI PIDNPDINPN SQHPTQQSTE SLTLYPTSSV SSSETEPAST
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FIGURE 20

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NL/24/01 (.  ESEHHTSSPP TESNKETSTI PIDNPDINPN SQHPTQQSAE SLTLYPTSSV SSSETEPAST
NL/23/01 (    ESEHHTSSPP TESNKETSTI PIDNPDINPN SQHPTQQSTE SLTLYPTSSV SSSETEPAST
NL/29/01 (    ESEHHTSSPP TESNKEASTI STDNPDINPN SQHPTQQSTE NPTLNPAASA SPSETESAST
NL/3/02 (A    ESEHHTSSPP TESNKEASTI STDNPDINPN SQHPTQQSTE NPTLNPAASA SPSETESAST
NL/1/99 (p    KTENCANMPS AEPSKKTPMT STAGPNTKPN PQQATQWTTE NSTSPVATPE GHPYTGTTQT
NL/11/00 (    KTENCANMPS AEPSKKTPMT STAGPSTEPN PQQATQWTTE NSTSPAATLE SHPYTGTTQT
NL/12/00 (    KTENCANMPP AEPSKKTPMT STAGLNTKPN PQQATQWTTE NSTPPAATSE GHLHTGTTQT
NL/5/01 (B    KTENCANMPP AEPSKKTPMT STAGPNTKPN PQQATQWTTE NSTSPAATPE GHLHTGTTQT
NL/9/01 (B    KTENCANMPP AEPSKKTPMT STAGLNTKPN PQQATQWTTE NSTSPAATPE GHLHTGTTQT
NL/21/01 (    KTENCANMPP AEPSKKTPMT STAGPNTKPN PQQATQWTTE NSTSPAATPE GHLHTGTTQT
NL/1/94 (p    KVEHCVNMPP VEPSKKTPMT SAVDLNTKPN PQQATQLAAE DSTSLAATSE DLLHTGTTPT
NL/1/82 (B    KVEHCANMPP VEPSKKTPMT STVDSSTGPN PQQTTQWTTE DSTSLAATSE DLHTGTTPPT
NL/1/96 (B    KVEHCVNMPP VEPSKKTPMT SAVDLNTKLN PQQATQLTTE DSTSLAATSE DHLLTGTTPPT
NL/6/97 (B    KVEHCVNMPP VEPSKKTPMT SAVDLNTKLN PQQATQLTTE DSTSLAATSE GHPHTGTTPPT
NL/9/00 (B    KVEHCVNMPP VEPSKKTPMT SAVDSNTKPN PQQATQLTTE DSTSLAATLE GHLHTGTTPPT
NL/3/01 (B    RVEHCVNMPP VEPSKKTPMT SAVDLNTKPN PQRATQLTTE DSTSLAATLE GHLHTGTTPPT
NL/4/01 (B    RVEHCVNMPP VEPSKKTPMT SAVDLNTKPN PQQATQLTTE DSTSLAATLE GHLHTGTTPPT
UK/5/01 (B    KVEHCVNMPP VEPSKKTPMT SAVDLNTKPN PQQATQLTTE DSTSLAATLE DHPHTGTTPT
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              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
NL/1/00 (p    PDTTNRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRTSSR- -----THSPP RATTRTARRT
BR/2/01 (A    PDTTNRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRTSSR- -----THSPP RATTRTARRT
FL/4/01 (A    PDTTNRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRISSR- -----THSPP WATTRTARRT
FL/3/01 (A    PDTTDRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRISSR- -----THSPP WATTRTARRT
FL/8/01 (A    PDDTDRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRISSR- -----THSPP WATTRTART
FL/10/01 (    PDTTSRPPFV DTHTTPPSAS RTKTSPAVHT KNNPRVSPR- -----THSPP WATTRTART
NL/10/01 (    PDTTSRPPFV DTHTTPPSAS RIRTSPAVHT KNNLRISPR- -----THSPP WAMTRTVRGT
NL/2/02 (A    PDTTSRPPFV DTHTTPSSAS RIRTSPAVHT KNNLRISPR- -----THSPP WAMTRTVRGT
NL/17/00 (    PDTTNRLSSV DRSTAQPSES RTKTKPTVHT INNPNTASS- -----TQSPP RTTTKAIRRA
NL/1/81 (A    PDTTNRLSSV DRSTTQPSES RTKTKPTVHT KNNPSTVSR- -----TQSPL RATTKAVLRA
NL/1/93 (A    PDTTNRLSSA DRSTTQPSES RTKTKLTVHT KNNLSTASR- -----TQSPP RATTKAVLRD
NL/2/93 (A    PDTTNRLSSA DRSTTQPSES RTKTKLTVHT KNNLSTASR- -----TQSPP RATTKAVLRD
NL/3/93 (A    PDTTNRLSSV DRSTTQPSES RTKTKLTVHK KNIPSTVSR- -----TQSSI RATTKAVLRA
NL/1/95 (A    SDTTSRLSSV DRSTTQPSES RARTKPTVHK KNIPSTVSR- -----TQSPL RATTKAVLRA
NL/2/96 (A    PDTTNRLSSV DRSTAQPSES RTKTKPTVHK KNIPSTVSR- -----TQSPP RVTTKAILRA
NL/3/96 (A    SDTTNRLSSV DRSTTQPSES RARTKPTVHK KNIPSTVSR- -----TQSPL RATTKAVLRA
NL/22/01 (    PGITNHLSFV DRSTTQPSES RTKTNRTVHK KNISSTVSR- -----TQSPP RTTAKAVPRA
NL/24/01 (    PGITNHLSFV DRSTTQPSES RTKTNRTVHK KNISSTVSR- -----TQSPP RTTAKAVPRA
NL/23/01 (    PGITNHLSFV DRSTTQPSES RTKTNRTVHK KNISSTVSR- -----TQSPP RTTAKAVPRA
NL/29/01 (    PDTTNRLSSV DRSTVQPSEN RTKTKLTVHT RNNLSTASS- -----TQSPP RATTKAIRRA
NL/3/02 (A    PDTTNRLSSV DRSTVQPSEN RTKTKLTVHT RNNLSTASS- -----TQSPP RATTKAIRRA
NL/1/99 (p    SDTTAPQQTT DKHTAPLKST NEQITQTTTE KKTIRATTQK REKGKENTNQ TTSTAATQTT
NL/11/00 (    PDITAPQQTT DKHTALPKST NEQITQTTTE KKTTRATTQK REKEKENTNQ TTSTAATQTT
NL/12/00 (    PDTTAPQQTT DKHTALPKST NEQITQTTTE KKTTRATTQR REKGKENTNQ TTSTAATQTT
NL/5/01 (B    PDTTAPQQTT DKHTALPKST NEQITQATTE KKTTRETTQR REKGKENTNQ TTSTAATQTT
NL/9/01 (B    PDTTAPQQTT DKHTALPKST NEQITQTTTE KKTTRATTQR REKGKENTNQ TTSTAATQTT
NL/21/01 (    PDTTAPQQTT DKHTALPKST NEQITQTTTE KKTTRATTQR REKGKENTNQ TTSTAATQTT
NL/1/94 (p    PDATVSQQTT DEYTTLLRST NGQTIQTTTE KKPTGATTK- -----KETTN TTSTAATQTL
NL/1/82 (B    LDATVSQQTT DKHTTPLRST NGQTIQTTTE KKPTARAIAK- -----KETTN TTSTAATQTF
NL/1/96 (B    PDATVSQQTT DEHTTLLRST NRQTTQTATE KKPTGATTK- -----KETTIR TTSTAATQTP
NL/6/97 (B    PDATVSQQTT DEHTTLLRST NRQTTQTATE KKPTGATTK- -----KETTIR TTSTAATQTP
NL/9/00 (B    PDATVSQQTT DEHTTLLRST NRQTTQTTAE KKPTRATTK- -----KETTIR TTSTAATQTL
NL/3/01 (B    PDVTVSQQTT DEHTTLLRST NRQTTQTAAE KKPTRVTTN- -----KETTIR TTSTAATQTL
NL/4/01 (B    PDATVSQQTT DEHTTLLRST NRQTTQTTAE KKPTRATTK- -----KETTIR TTSTAATQTL
UK/5/01 (B    PDATVSQQTT DEHTTLLRST NRQTTQTTAE KKPTRATTK- -----KETTTR TTSTAATQTL
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              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
NL/1/00 (p    TTLRTSSTRK RPSTASVQPD ISATTHKNEE ASPASPQTSA STTRIQRKSV EANTSTTYNQ
BR/2/01 (A    TTLRTSSTRK RPSTASVQPD ISATTHKNEE ASPASPQTSA STTRIQRKSV EANTSTTYNQ
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FL/4/01  (A   TTLRTSSTRK RPSTASAQPD ISATTHKNEE ASPASPQTSA STTRTQRKSV EANTSTTYNQ
FL/3/01  (A   TTLRTSSTRK RPSTASVQPD ISATTHKNEE ASPASPQTSA STTRTQRKSV EANTSTTYNQ
FL/8/01  (A   TTLRTSSTRK RPSTASVQPD ISATTHKNEE ASPASPQTSA STTRTQRKSV EANTSTTYNQ
FL/10/01 (    TTLRTSSTRK RLSTASVQPD SSATTHKHEE TSPVSPQTSA STARPQRKGM EASTSTTYNQ
NL/10/01 (    TTLRTSSIRK RPSTASVQPD SSATTHKHEE ASPVSPQASA STARPQRKGM EASTSTTYNQ
NL/2/02  (A   TTLRTSSIRK RPSTASVQPD SSATTHKHEE ASPVSPQASA STARPQRKGM EASTSTTYNQ
NL/17/00 (    TTFRMSSTGK RPTTTLVQSD SSTTTQNHEE TGSANPQASA STMQN----- ----HTNNIK
NL/1/81  (A   TAFRTSSTRK RPTTTSVQSD SSTTTQNHEE TSSANPQASA STMQSQ---- ----HTNNIK
NL/1/93  (A   TAFHTSSTGK RPTTTSVQSG SSTTTQNHEE TSSSNPQASA STMQDQ---- ----DTNNTK
NL/2/93  (A   TAFHTSSTGK RPTTTSVQSG SSTTTQNHEE TSSSNPQASA STMQDQ---- ----DTNNTK
NL/3/93  (A   TAFRTSSTGK RPTTTSVQSD SSTTTQNHEE TGSANPQASA STMQN----- ----HTNIVK
NL/1/95  (A   TAFRTSSTGE GPTTTSVQSD SSTTTQNHEE TGSANPQASA STMQN----- ----HTNIVK
NL/2/96  (A   TVFRMSSTGK RPATTLVQSD SSTTTQNHEE TGSANSQASA STMQN----- ----HSNNIK
NL/3/96  (A   TAFRMSSTGE GPTTTSVQSD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNIAK
NL/22/01 (    TALRTSSTGE RPTTTPVQPD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNIAR
NL/24/01 (    TALRTSSTGE RPTTTPVQPD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNIAR
NL/23/01 (    TALRTSSTGE RPTTTPVQPD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNIAR
NL/29/01 (    TTLRMSSTGR RPTTTLVQSD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNNIK
NL/3/02  (A   TTLRMSSTGR RPTTTLVQSD SSTTTQNHEE TGSANPQASA STMQNQ---- ----HTNNIK
NL/1/99  (p   NTTNQIRNAS ETITTSDRPR TDTTTQSSEQ TTRATDPSSP PHHAR----- ----GAKLK-
NL/11/00 (    NTTNQTRNAS ETITTSDRPR IDTTTQSSEQ TTRATDPSSP PHHAQS---- ----GAKPK-
NL/12/00 (    NTTNQIRNAS ETITTSDRPR TDSTTQSSEQ TTRATDPSSP PHHAQG---- ----SAKPK-
NL/5/01  (B   NTTNQIRNAS ETITTSDRPR TDSTTQSSEQ TTQATDPSSP AHHAQQ---- ----SAKPK-
NL/9/01  (B   NTTNQIRNAS ETITTSDRPR TDSTTQSSEQ TTRATDPSSP PHHAQQ---- ----SAKPK-
NL/21/01 (    NTTNQIRNAI ETITTSDRPR TDSTTQSSEQ TTRATDPSSH PHHAQQ---- ----SAKPK-
NL/1/94  (p   NTTNQTSYVR EATTTSARSR NSATTQSSDQ TTQAADPSSQ PHHTQK---- ----STTTTY
NL/1/82  (B   NTTNQTRNGR ETTITSARSR NDATTQSSEQ TNQTTDPSSQ PHHAIS---- ----TITITQ
NL/1/96  (B   NTTNQTSNGR EATTTSTRSR NGATTQNSDQ TT-TADPSSQ PHHTQK---- ----STTTTY
NL/6/97  (B   NTTNQTSNGR EATTTSARSR NGATTQNSDQ ITQAADSSSQ PHHTQK---- ----STTTAY
NL/9/00  (B   NTTNQTSNGR EATTTSARSR NNATTQSSDQ TTQAAEPSSQ SQHTQK---- ----STTTTY
NL/3/01  (B   NTTNQTNNGR EATTTSARSR NNATTQSSDQ TTQAADPSSQ SQHTQK---- ----SITTTY
NL/4/01  (B   NTTNQTSNGR EATTTSARSR NNATTQSSDQ TTQAADPSSQ SQHTKK---- ----STTTTY
UK/5/01  (B   NTTNQTSNGR EATTTSARSR NNATTQSSDQ TTQAAEPNSQ SQHTQK---- ----STTTTY

                           ....|....
                             245
NL/1/00  (p   TS-------
BR/2/01  (A   TS-------
FL/4/01  (A   TS-------
FL/3/01  (A   TS-------
FL/8/01  (A   TS-------
FL/10/01 (    TS-------
NL/10/01 (    TS-------
NL/2/02  (A   TS-------
NL/17/00 (    PN-------
NL/1/81  (A   PN-------
NL/1/93  (A   QN-------
NL/2/93  (A   QN-------
NL/3/93  (A   PN-------
NL/1/95  (A   PN-------
NL/2/96  (A   PN-------
NL/3/96  (A   PN-------
NL/22/01 (    PN-------
NL/24/01 (    PN-------
NL/23/01 (    PN-------
NL/29/01 (    PN-------
NL/3/02  (A   PN-------
NL/1/99  (p   ---------
NL/11/00 (    ---------
NL/12/00 (    ---------
NL/5/01  (B   ---------
```

```
NL/9/01 (B .   ---------
NL/21/01 (     ---------
NL/1/94 (p     NTDTSSPSS
NL/1/82 (B     HRHIFSK--
NL/1/96 (B     NTDTSSPSS
NL/6/97 (B     NTDTSFPSS
NL/9/00 (B     NTDTSSLSS
NL/3/01 (B     NTDTSSPSS
NL/4/01 (B     NTDTSSPSS
UK/5/01 (B     NTDTSSLSS
```

Phylogenetic analysis of hMPV F sequences
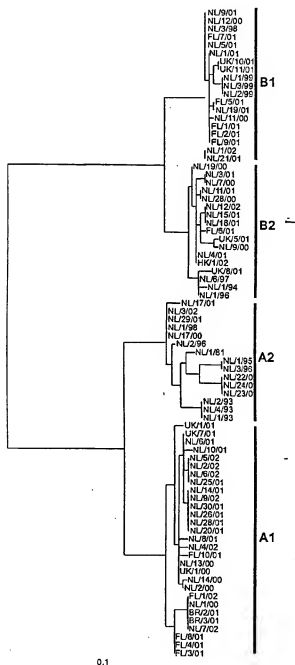
FIGURE 21

Phylogenetic analysis of G sequences
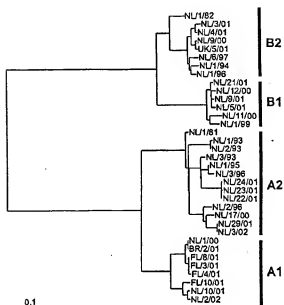
FIGURE 22

Growth Curve for hMPV001 in Vero Cells
MOI = 0.1

FIGURE 23

Accl

```
CATATTGTAATACGACTCACTATAGGACGGCAAAAAACCGTATACATCCAATTATAATTTCTTATTTTTAATAAA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 76
GTATAACATTATGCTGAGTGATATCCTGCCGTTTTTTTGGCATATGTAGGTTAATATTAAAGAATAAAAATTATTT
```

◄━━━━━━━ P-T7 ━━━━━━━►┃   ━━━━━━━━━ Tr

PacI

```
CTTAATGACAGTTGTTAGTTTCTAACTTTTGATTTTTAGTTTTTAATTAACTATTACATAATTGCATAATCAAATG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 152
GAATTACTGTCAACAATCAAAGATTGAAAACTAAAAATCAAAAATTAATTGATAATGTATTAACGTATTAGTTTAC
```

━━━━━━━━━━━━━━━━━━━━━━━ Tr ━━━━━━━━━━━━━━━━━━

```
ATTACTTTGGAATAGTATGAAGTTGTCACCTATTTTATCATTTTTATCATTTTTTACGCGCCGCCCTGCCACTCAT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 228
TAATGAAACCTTATCATACTTCAACAGTGGATAAAATAGTAAAAATAGTAAAAAATGCCGGCGGGACGGTGAGTA
```

━━━━━━━━━ Tr ━━━━━━━━┃   . A   G   G   Q   W   E   D
                                              └──── CAT ────

Scal

```
CGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACCTGAATCGC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 304
GCGTCATGACAACATTAAGTAATTCGTAAGACGGCTGTACCTTCGGTAGTGTTTGCCGTACTACTTGGACTTAGCG
```

  C   Y   Q   Q   L   E   N   L   M   R   G   V   H   F   G   D   C   V   A   H   H   H   V   Q   I   A
  ─────────────────────────────────────── CAT ───────────────────────────────

                              Sspl   NcoI

```
CAGCGGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGGGCGAAGAAGTTGTCCATA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 380
GTCGCCGTAGTCGTGGAACAGCGGAACGCATATTATAAACGGGTACCACTTTTGCCCCCGCTTCTTCAACAGGTAT
```

  L   P   M   L   V   K   D   G   Q   T   Y   Y   K   G   M   T   F   V   P   A   F   F   N   D   M
  ─────────────────────────────────────── CAT ───────────────────────────────

    MscI   DraI   BsmBI

```
TTGGCCACGTTTAAATCAAAACTGGTGAAACTCACCCAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 456
AACCGGTGCAAATTTAGTTTTGACCACTTTGAGTGGGTCCCTAACCGACTCTGCTTTTGTATAAGAGTTATTTGG
```

  N   A   V   N   L   D   F   S   T   F   S   V   W   P   N   A   S   V   F   F   M   N   E   I   F   G
  ─────────────────────────────────────── CAT ───────────────────────────────

FIGURE 24

```
CTTTAGGGAAATAGGCCAGGTTTTCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 532
GAAATCCCTTTATCCGGTCCAAAAGTGGCATTGTGCGGTGTAGAACGCTTATATACACATCTTTGACGGCCTTTAG

   K  P  F  Y  A  L  N  E  G  Y  C  A  V  D  Q  S  Y  I  H  L  F  Q  R  F  D
                                     CAT
```

```
GTCGTGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAAGGGTGAACACTA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 608
CAGCACCATAAGTGAGGTCTCGCTACTTTTGCAAAGTCAAACGAGTACCTTTTGCCACATTGTTCCCACTTGTGAT

   D  H  Y  E  S  W  L  S  S  F  T  E  T  Q  E  H  F  V  T  Y  C  P  H  V  S
                                   CAT
```

EcoRI

```
TCCCATATCACCAGCTCACCGTCTTTCATTGCCATACGGAATTCCGGATGAGCATTCATCAGGCGGGCAAGAATGT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 684
AGGGTATAGTGGTCGAGTGGCAGAAAGTAACGGTATGCCTTAAGGCCTACTCGTAAGTAGTCCGCCCGTTCTTACA

   D  W  I  V  L  E  G  D  K  M  A  M  R  F  E  P  H  A  N  M  L  R  A  L  I  H
                                      CAT
```

                                    DraI   PvuII

```
GAATAAAGGCCGGATAAAACTTGTGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 760
CTTATTTCCGGCCTATTTTGAACACGAATAAAAAGAAATGCCAGAAATTTTTCCGGCATTATAGGTCGACTTGCCA

   I  F  A  P  Y  F  K  H  K  N  K  K  V  T  K  L  F  A  T  I  D  L  Q  V  T
                                     CAT
```

```
CTGGTTATAGGTACATTGAGCAAGTGACTGAAATGCCTCAAAATGTTCTTTACGATGCGATTGGGATATATCAACG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 836
GACCAATATCCATGTAACTCGTTCACTGACTTTACGGAGTTTTACAAGAAATGCTACGCTAACCCTATATAGTTGC

   Q  N  Y  T  C  Q  A  L  S  Q  F  A  E  F  H  E  K  R  H  S  Q  S  I  D  V
                                      CAT
```

                                                              AflIII
              AccI   MluI

```
GNGGTATACCCAGTGATTTTTTTCTCCATTTTCACTTGTCCCATATTTTTTTGGAATCTAATTTATACGCGTTTTT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+---- 912
CNCCATATGGGTCACTAAAAAAAGAGGTAAAAGTGAACAGGGTATAAAAAAACCTTAGATTAAATATGCGCAAAAA

   ?  T  Y  G  T  I  K  K  E  M                        Le+AC
                    CAT
```

```
                                           KasI
                NgoMIV                      NgoMIV
TTCGCGTGGCCGGCATGGTCCCAGCCTCCTCGCTGGCGCCGGCTGGGCAACATTCCGAGGGGACCGTCCCCTCGGT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 988
AAGCGCACCGGCCGTACCAGGGTCGGAGGAGCGACCGCGGCCGACCCGTTGTAAGGCTCCCCTGGCAGGGGAGCCA

■Le+AC ■                                              ■Hep-d Ribo■
```

```
          BamHI
AATGGCGAATGGGACGGATCCGGCTGCTAACAAAGCCCGAAA
+----+----+----+----+----+----+----+----+---→ 1030
TTACCGCTTACCCTGCCTAGGCCGACGATTGTTTCGGGCTTT

■■Hep-d Ribo■■        ■━━━T-T7━━━■
```
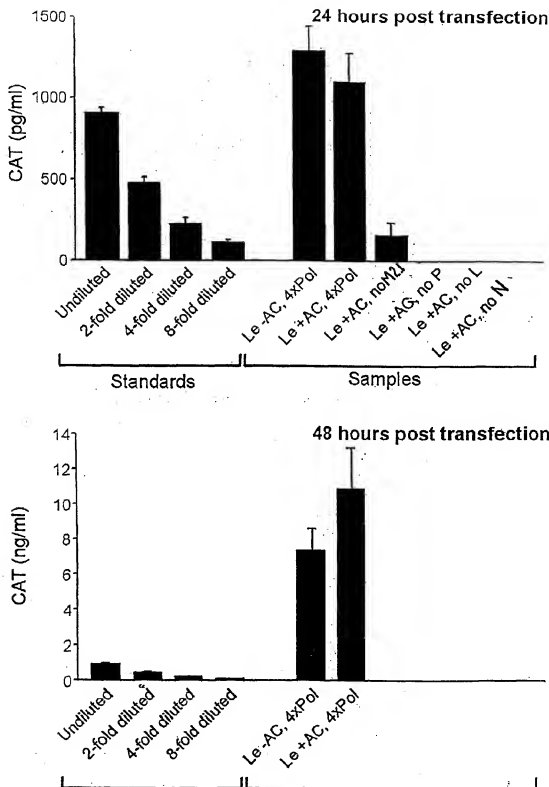
FIGURE 25

Leader and Trailer Sequence Comparison

```
hMPV le  ACG CGA AAA AAA C  GC GTA TA
hMPV tr  TGC    TTT TTT G  GC ATA T

APV le   ACG AGA AAA AAA C  GC ATT CAA GCA GG
APV tr   TGC TCT TTT TTT G  GC ATA AGT AGT TT

RSV A2 le ACG GGA AAA AAT GCG TAC AAC AAA CTT
RSV A2 tr TGC TCT TTT TTT CAC AGT TTT T

BRSV le  ACG CGA AAA AAT GCG TAT AAC AAA CCT GT
BRSV tr  TGC TCT TTT TTT CAT AGT TTT TG

HPIV3 le  ACC AAA CAA GAG AAG A  GA CTT
HPIV3 tr  TGG TTT GTT CTC TTC T  TG AGA

BPIV3 le  ACC AAA CAA GAG AAG A  GA CTT
BPIV3 tr  TGG TTT GTT CTC TTT T  TG AGA
```

Yellow color are non-complementary nucleotides between leader and trailer sequences

Green color is a nucleotide to be tested next: change C -> A, or G
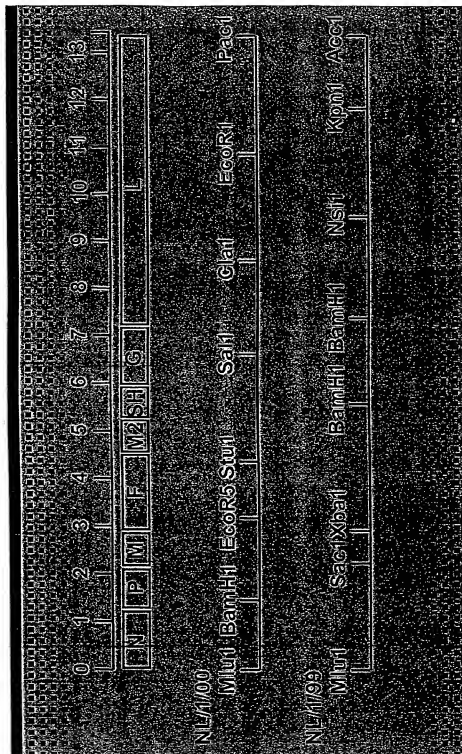
FIGURE 26

FIGURE 27

FIGURE 28
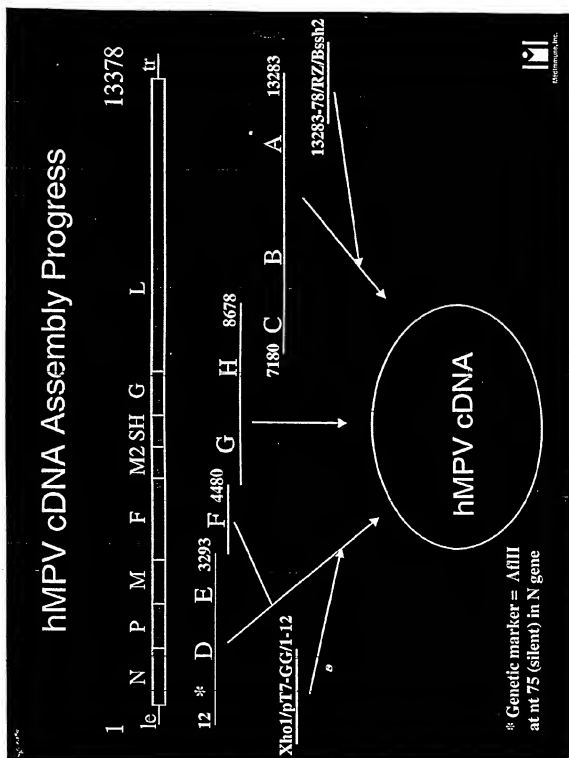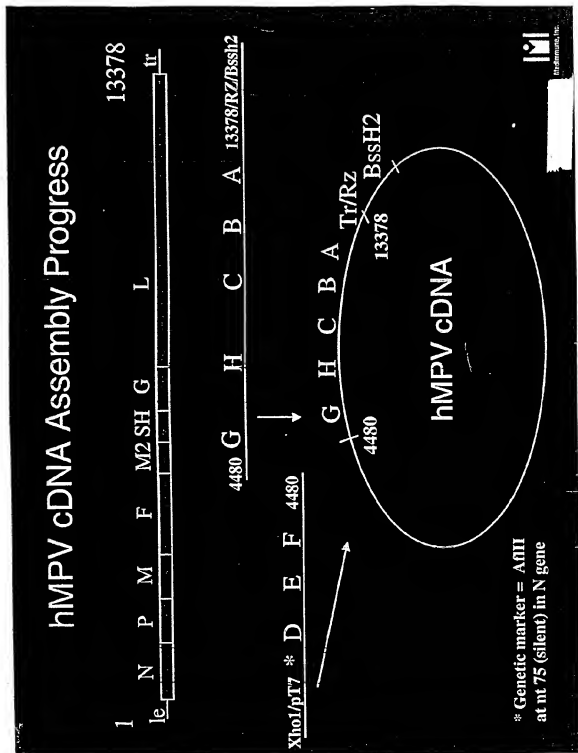
FIGURE 29A

FIGURE 29B

FIGURE 30

FIGURE 30   contd.

FIGURE 30   contd.
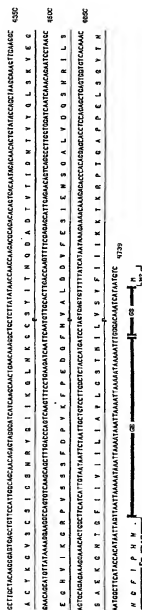
FIGURE 31 A

FIGURE 31 B

+ = positive; - = negative; T = throatswabs; NO = nose swab; N = not done; ? = not sure;
D = dead; 0 to 12: days post infection. 2e infection is only tested on nose swabs.

nr	1e infection	swab	0	1	2	3	4	5	8	10	11	12	2e infection	0	1	2	3	4	5
1	00-1	T	-	+	+	+	-	+	+	+	-	-	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
2	00-1	T	-	+	+	+	+	+	-	-	-	D		N	N	N	N	N	N
		NO		+	+	+	+	-	+	N	+	-	D	-	-	-	-	-	-
3	00-1	T	-	-	?	-	-	-	-	-	-	N	99-1	N	N	?	N	N	N
		NO		+	?	?		-	N	-	-	-		-	-	?	+	+	-
4	00-1	T	-	+	+	+	+	-	+	-	?	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	?	-	-		-	-	-	+	-	-
5	00-1	T	-	?	+	+	+	+	+	+	-	N	00-1	N	N	N	N	N	N
		NO		+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
6	00-1	T	-	-	+	+	+	+	-	+	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	+	?		-	-	-	-	-	-
7	99-1	T	-	-	-	+	+	-	+	D	-	N		N	N	N	N	N	N
		NO	-	-	-	+	+	+	N	D	-	-		-	-	-	-	-	-
8	99-1	T	-	-	+	+	-	-	-	-	N	00-1	N	N	N	N	N	N	N
		NO	-	?	-	+	+	?	N	-	-			-	-	+	+	+	+
9	99-1	T	-	-	-	-	-	-	-	-	N	00-1	N	N	N	N	N	N	N
		NO	-	-	-	-	+	+	N	-	-			-	?	+	+	-	-
10	99-1	T	-	-	-	+	+	-	-	-	N	99-1	N	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-			-	-	-	-	-	-
11	99-1	T	-	-	+	+	+	-	-	-	N	99-1	N	N	N	N	N	N	N
		NO	-	+	?	+	+	+	N	-	-			-	-	-	+	-	-
12	99-1	T	-	-	+	+	?	-	-	-	N	99-1	N	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-			-	-	-	-	-	-

FIGURE 32
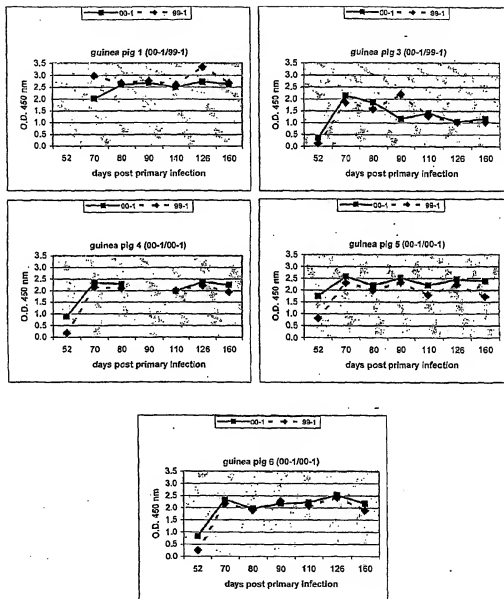
FIGURE 33A
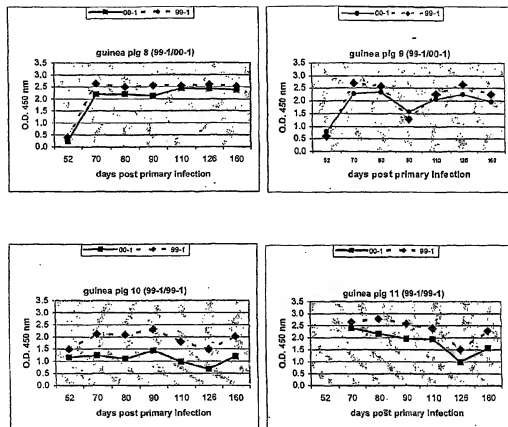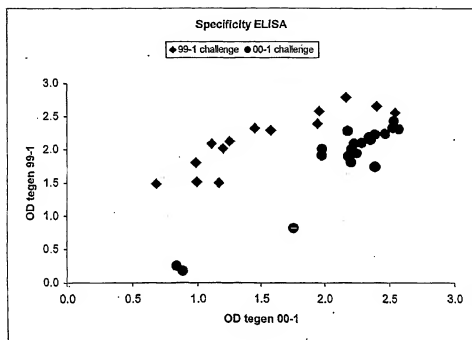
FIGURE 33B
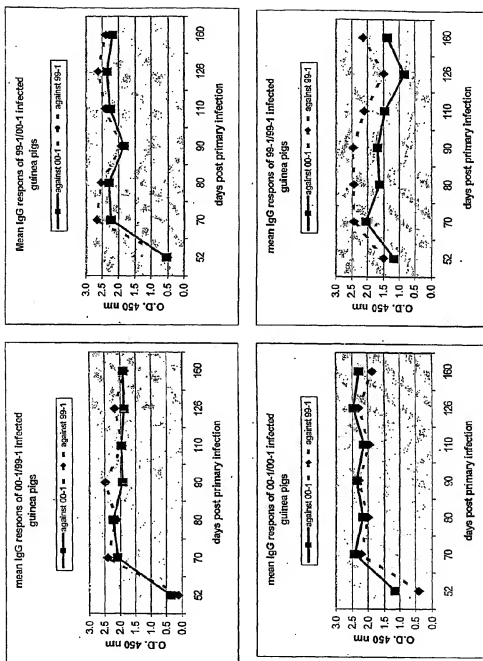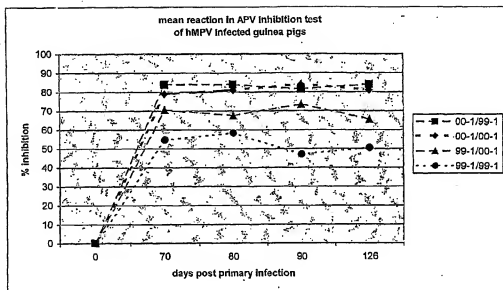
FIGURE 34

FIGURE 35

FIGURE 36

	Against 00-1	Against 99-1	Against APV-C
1 infection with 00-1	20-60	< 10	< 10
2 infections with 00-1	>320-1280	40-80	< 10-60
1 infection with 99-1	<10-60	10-80	< 10
2 infections with	20-40	80-400	<10-40

FIGURE 37

+ = positive; - = negative; N = not done; ? = not sure; 0 to 10: days post infection

nr	1st infection	0	2	3	4	5	6	7	8	9	11	2nd infection	0	1	2	3	4	5	7	10
3	00-1	-	-	-	+	+	+	+	+	N	-		-	+	+	+	+	-	?	-
6	00-1	-	+	+	+	+	+	+	-	-	-		-	+	+	+	+	+	-	-

FIGURE 38

FIGURE 39A

FIGURE 39B

Correlation between APV and hMPV ELISA for the detection of hMPV IgG antibodies in human sera

$y = 0.7507x + 0.1759$
$R^2 = 0.7953$
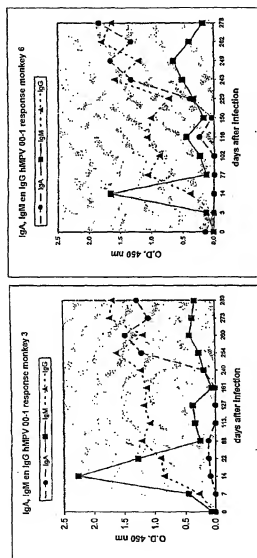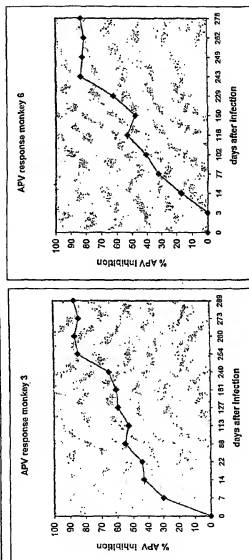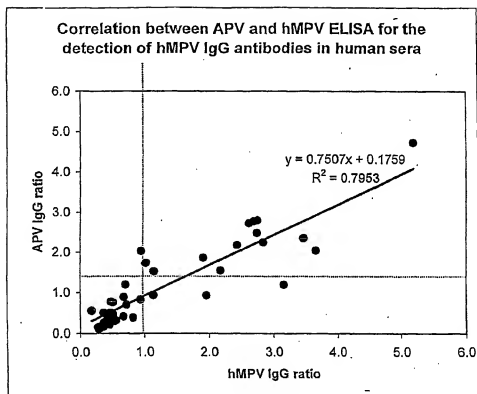
FIGURE 40

FIGURE 41

Comparison of two prototypic hMPV isolates with APV-A and APV-C

DNA similarity matrices

```
N  00-1  99-1  APVC  APVA
00-1  1,000 0,862 0,757 0,660
99-1  ---   1,000 0,757 0,663
APVC  ---   ---   1,000 0,656
APVA  ---   ---   ---   1,000


P  00-1  99-1  APVC  APVA
00-1  1,000 0,811 0,677 0,588
99-1  ---   1,000 0,674 0,593
APVC  ---   ---   1,000 0,584
APVA  ---   ---   ---   1,000


M  00-1  99-1  APVC  APVA
00-1  1,000 0,865 0,766 0,695
99-1  ---   1,000 0,773 0,707
APVC  ---   ---   1,000 0,705
APVA  ---   ---   ---   1,000


F  00-1  99-1  APVC  APVA
00-1  1,000 0,838 0,706 0,662
99-1  ---   1,000 0,716 0,655
APVC  ---   ---   1,000 0,685
APVA  ---   ---   ---   1,000


M2-1  00-1  99-1  APVC  APVA
00-1  1,000 0,863 0,764 0,668
99-1  ---   1,000 0,744 0,657
APVC  ---   ---   1,000 0,670
APVA  ---   ---   ---   1,000


M2-2  00-1  99-1  APVC  APVA
00-1  1,000 0,861 0,648 0,486
99-1  ---   1,000 0,675 0,486
APVC  ---   ---   1,000 0,463
APVA  ---   ---   ---   1,000


SH 00-1  99-1  APVC  APVA
00-1  1,000 0,688 N.A.  0,421
99-1  ---   1,000 N.A.  0,380
APVC  ---   ---   N.A.  N.A.
APVA  ---   ---   ---   1,000


G  00-1  99-1  APVC  APVA
00-1  1,000 0,543 N.A.  0,262
99-1  ---   1,000 N.A.  0,263
APVC  ---   ---   N.A.  N.A.
APVA  ---   ---   ---   1,000
```

	00-1	99-1	APVC	APVA
5'L				
00-1	1,000	0,835	N.A.	0,596
99-1	---	1,000	N.A.	0,605
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 1500 nucleotides of 99-1 were available.
N.A.: sequence not available.

Protein similarity matrices

```
N 00-1   99-1   APVC   APVA
00-1    1,000  0,949  0,880  0,685
99-1     ---   1,000  0,883  0,682
APVC     ---    ---   1,000  0,700
APVA     ---    ---    ---   1,000

P 00-1   99-1   APVC   APVA
00-1    1,000  0,860  0,683  0,552
99-1     ---   1,000  0,676  0,549
APVC     ---    ---   1,000  0,528
APVA     ---    ---    ---   1,000

M 00-1   99-1   APVC   APVA
00-1    1,000  0,976  0,874  0,775
99-1     ---   1,000  0,874  0,763
APVC     ---    ---   1,000  0,775
APVA     ---    ---    ---   1,000

F 00-1   99-1   APVC   APVA
00-1    1,000  0,938  0,810  0,677
99-1     ---   1,000  0,803  0,674
APVC     ---    ---   1,000  0,719
APVA     ---    ---    ---   1,000

M2-1     00-1   99-1   APVC   APVA
00-1    1,000  0,946  0,844  0,719
99-1     ---   1,000  0,834  0,703
APVC     ---    ---   1,000  0,704
APVA     ---    ---    ---   1,000

M2-2     00-1   99-1   APVC   APVA
00-1    1,000  0,901  0,563  0,246
99-1     ---   1,000  0,577  0,232
APVC     ---    ---   1,000  0,191
APVA     ---    ---    ---   1,000

SH       00-1   99-1   APVC   APVA
00-1    1,000  0,570  N.A.   0,178
99-1     ---   1,000  N.A.   0,162
APVC     ---    ---   N.A.   N.A.
APVA     ---    ---    ---   1,000

G 00-1   99-1   APVC   APVA
00-1    1,000  0,326  N.A.   0,094
99-1     ---   1,000  N.A.   0,107
APVC     ---    ---   N.A.   N.A.
APVA     ---    ---    ---   1,000

5'L      00-1   99-1   APVC   APVA
00-1    1,000  0,921  N.A.   0,600
99-1     ---   1,000  N.A.   0,594
APVC     ---    ---   N.A.   N.A.
APVA     ---    ---    ---   1,000
```

5'L: only the first 500 amino acid residues of 99-1 were
available.
N.A.: sequence not available.

FIGURE 42A

Comparison of the coding sequences of 4 hMPV prototypes

N nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.938	0.864	0.854
NL/17/00		0.870	0.861
NL/1/99			0.944

N aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.994	0.954	0.961
NL/17/00		0.956	0.964
NL/1/99			0.984

P nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.923	0.812	0.818
NL/17/00		0.807	0.811
NL/1/99			0.932

P aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.955	0.863	0.867
NL/17/00		0.857	0.863
NL/1/99			0.959

M nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.938	0.860	0.861
NL/17/00		0.848	0.852
NL/1/99			0.942

M aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.988	0.976	0.976
NL/17/00		0.972	0.972
NL/1/99			1.000

F nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.937	0.840	0.840
NL/17/00		0.838	0.840
NL/1/99			0.943

F aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.979	0.940	0.946
NL/17/00		0.942	0.949
NL/1/99			0.987

M2 nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.943	0.854	0.854
NL/17/00		0.863	0.851
NL/1/99			0.943

M2.1 nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.943	0.863	0.861
NL/17/00		0.870	0.852
NL/1/99			0.939

M2.1 aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.983	0.948	0.951
NL/17/00		0.951	0.957
NL/1/99			0.978

M2.2 nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.953	0.861	0.865
NL/17/00		0.870	0.875
NL/1/99			0.967

M2.2 aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.957	0.901	0.915
NL/17/00		0.887	0.901
NL/1/99			0.985

SH nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.884	0.682	0.673
NL/17/00		0.688	0.685
NL/1/99			0.887

SH aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.836	0.570	0.576
NL/17/00		0.805	0.622
NL/1/99			0.830

G nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.762	0.530	0.575
NL/17/00		0.573	0.546
NL/1/99			0.765

G aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.652	0.309	0.341
NL/17/00		0.337	0.338
NL/1/99			0.651

L nt	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.944	0.843	0.843
NL/17/00		0.843	0.843
NL/1/99			0.952

L aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.986	0.942	0.938
NL/17/00		0.944	0.939
NL/1/99			0.985

FIGURE 42B

Amino acid sequence alignment of two prototype hMPV isolates

Nucleoprotein (N)

```
            10        20        30        40        50        60
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGEILYSKHRDYK 60
99-1  MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGEILYSKHRDYK 60

            70        80        90       100       110       120
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  YAAEIGIQYISTALGSERVQQILRNSGSEVQVVLTRTYSLGKSKNNKGEDLQMLDIHGVE 120
99-1  YAAEIGIQYISTALGSERVQQILRNSGSEVQVVLTKTYSLGKSKNSKGEELQMLDIHGVE 120

           130       140       150       160       170       180
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  KSWVEEIDKEARKTMATLLKESSGNIPQNQRPSAPDTPIILLCVGALIFTKLASTIEVGL 180
99-1  KSWIEEIDKEARKTMVTLLKESSGNIPQNQRPSAPDTPIILLCVGALIFTKLASTIEVGL 180

           190       200       210       220       230       240
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  ETTVRRANRVLSDALKRYPRMDIPKIARSFYDLFEQKVYHRSLFIEYGKALGSSSTGSKA 240
99-1  ETTVRRANRVLSDALKRYPRIDIPKIARSFYELFEQKVYYRSLFIEYGKALGSSSTGSKA 240

           250       260       270       280       290       300
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  ESLFVNIFMQAYGAGQTMLRWGVIARSSNNIMLGHVSVQABLKQVTEVYDLVREMGPESG 300
99-1  ESLFVNIFMQAYGAGQTLLRWGVIARSSNNIMLGHVSVQSELKQVTEVYDLVREMGPESG 300

           310       320       330       340       350       360
   ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LLHLRQSPKAGILSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSAAESYAKSLKE 360
99-1  LLHLRQSPKAGILSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSAAESYARSLKE 360

           370       380       390
   ....|....|....|....|....|....|....
00-1  SNKINFSSLGLTDEEKEAAEHFLNVSDDSQNDYE 394
99-1  SNKINFSSLGLTDEEKEAAEHFLNMSGDNQDDYE 394
```

FIGURE 43

Phosphoprotein (P)

```
                 10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MSFPEGKDILFMGNEAAKIAEAFQKSLRKGGHKRSQSIIGEKVNTVSETLELPTISRPAK 60
99-1  MSFPEGKDILFMGNEAAKIAEAFQKSLKKSGHKRTQSIVGEKVNTISETLELPTISKPAR 60

                 70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  ETLTSEPKLAWTDKGGAIKTEIKQAIKVMDPIEEEESTEKKVLPSSDGKTPAEKKLKEST 120
99-1  SSTLTEPKLAWADNSGTKTITEKSAHKIMDFVEEEBFNEKKVLPSSDGKTPAEKKSMEST 120

                130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  NIIKKKVSFTENEPGKYTKLEKDALDLLSDNEEEDAESSILTFEERDTSSLSIEARLESIE 180
99-1  SVKKKKVSFTSNEPGKYTKLEKDALDLLSDNEEEDAESSILTFEEKDTSSLSIEARLESIE 180

                190       200       210       220       230      ·240
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGVREELIADIIKEAKGKAAEMMEEEMSQ 240
99-1  EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGIREELIAEIIKEAKGKAAEMMEEEMNQ 240

                250       260       270       280       290
          ....|....|....|....|....|....|....|....|....|....|....
00-1  RSKIGNGSVKLTEKAKELNKIVEDESTSGESEEEEEPKDTQDNSQEDIYQLIM 294
99-1  RSKIGNGSVKLTEKAKELNKIVEDESTSGESEEEEEPKETQDNNQEDIYQLIM 294
```

FIGURE 44

Matrix protein (M)

```
                   10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      MESYLVDTYQGIPYTAAVQVDLIEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL 60
99-1      MESYLVDTYQGIPYTAAVQVDLVEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL 60

                   70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      YAASQNGPILKVNASAQGAAMSVLPKKFEVNATVALDEYSKLEFDKLTVCEVKTVYLTTM 120
99-1      YAASQNGPILKVNASAQGAAMSVLPKKFEVNATVALDEYSKLDFDKLTVCDVKTVYLTTM 120

                  130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNTPVTIPAFIKSVSIKESESATVEAA 180
99-1      KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNTPVTIPAFIKSVSIKESESATVEAA 180

                  190       200       210       220       230       240
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      ISSEADQALTQAKIAPYAGLIMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISKICK 240
99-1      ISSEADQALTQAKIAPYAGLIMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISRICK 240

                  250
          ....|....|....
00-1      TWSHQGTRYVLKSR 254
99-1      SWSHQGTRYVLKSR 254
```

FIGURE 45

Fusion protein (F)

```
                 10        20        30        40        50        60
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    MSWKVVIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC  60
99-1    MSWKVMIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC  60

                 70        80        90       100       110       120
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    ADGPSLIKTELDLTKSALRELRTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA  120
99-1    ADGPSLIKTELDLTKSALRELKTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA  120

                130       140       150       160       170       180
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    GVAIAKTIRLESEVNAIKNALKKTNEAVSTLGNGVRVLATAVRELKDFVSKNLTRAINKN  180
99-1    GIAIAKTIRLESEVNAIKGALKQTNEAVSTLGNGVRVLATAVRELKEFVSKNLTSAINRN  180

                190       200       210       220       230       240
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQ  240
99-1    KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSYMPTSAGQ  240

                250       260       270       280       290       300
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    IKLMLENRAMVRRKGFGLIGVYGSSVIYMVQLPIFGVIDTPCWIVKAAPSCSEKKGNYA  300
99-1    IKLMLENRAMVRRKGFGLIGVYGSSVIYMVQLPIFGVIDTPCWIIKAAPSCSEKNGNYA  300

                310       320       330       340       350       360
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    CLLREDQGWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYP  360
99-1    CLLREDQGWYCKNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSRECNINISTTNYP  360

                370       380       390       400       410       420
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNVGIIKQLNKGCSYITNQDADTVTI  420
99-1    CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNVGIIKQLEKGCSYITNQDADTVTI  420

                430       440       450       460       470       480
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    DNTVYQLSKVEGEQHVIKGRPVSSSFDPVKFPEDQFNVALDQVFESIENSQALVDQSNRI  480
99-1    DNTVYQLSKVEGEQHVIKGRPVSSSFDPIKFPEDQFNVALDQVFESIENSQALVDQSNRI  480

                490       500       510       520       530
        ....|....|....|....|....|....|....|....|....|....|....|...
00-1    LSSAEKGNTGFIIVIILIAVLGSTMILVSVFIIIKKTKKPTGAPPELSGVTNQGIPHN  539
99-1    LNSAEKGNTGFIIVVILVAVLGLTMISVSIIIIKKTRKPTGAPPELNGVTNGGIPHS  539
```

FIGURE 46

22K protein (M2-1)

```
            10        20        30        40        50        60
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MSRKAPCKYEVRGKCNRGSECKFNHNYWSWPDRYLLIRSNYLLNQLLRNTDRADGLSIIS 60
99-1  MSRKAPCKYEVRGKCNRGSDCKFNHNYWSWPDRYLLLRSNYLLNQLLRNTDKADGLSIIS 60

            70        80        90       100       110       120
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  GAGREDRTQDFVLGSTNVVQGYIDDNQSITKAAACYSLHNIIKQLQEVEVRQARDNKLSD 120
99-1  GAGREDRTQDFVLGSTNVVQGYIDDNQSITKAAACYSLHNIIKQLQETEVRQARDNKLSD 120

            130       140       150       160       170       180
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  SKHVALHNLVLSYMEMSKTPASLINNLKRLPREKLKKLAKLIIDLSAGAENDSSYALQDS 180
99-1  SKHVALHNLILSYMEMSKTPASLINNLKRLPREKLKKLARLIIDLSAGGDNDSSYALQDS 180


      ....|..
00-1  ESTNQVQ 187
99-1  ESTNQVQ 187
```

FIGURE 47

M2-2 protein (M2-2)

```
                10        20        30        40        50        60
       ....|....|....|....|....|....|....|....|....|....|....|....|
00-1   MTLHMPCKTVKALIKCSEHGPVFITIEVDDMIWTHKDLKEALSDGIVKSHTNIYNCYLEN 60
99-1   MTLHMPCKTVKALIKCSKHGPRFITIEADDMIWTHKELKEHLSDGIVKSHTNIYSCYLEN 60

                70
       ....|....|.
00-1   IEIIYVKRYLS 71
99-1   IEIIYVKIYLS 71
```

FIGURE 48

Short hydrophobic protein (SH)

```
                  10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MHTLDVIKSDGSSKTCHLLKKIIKQHSGKVLIVLKLILALLTFHVTITINYIKVENNLQ 60
99-1  MKTLDVIKSDGSSETCNQLKKIIKKHSGKVLIALKLILALLTFHATITVNYIKVENNLQ 60

                  70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  ICQSKYESDKKCSSNTTSVTAKTTLNHDITCYEKSLIQRYTNSAINSDTCWKINRNQC 119
99-1  ACQFKNESDKKVTKTNTTSNTIRPTPDEIVHHLKSLIQRHTNSVTKDSDTCWRIHKNCR 120

                 130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  TNIYWYKFLCFKSPDTKTNCDKLYDLCRNRPKPAWGVYHIVECHCIYTVKWKCVHYPTD 179
99-1  TNIKTYKFLCSGFTNSKGNDCEEPTALCDKKPKIIVEKHRKAECHCLHTHSWQCLHP--- 177

          ....
00-1  BTQS 183
99-1  ---- 177
```

FIGURE 49

Attachment glycoprotein (G)

```
                    10        20        30        40        50        60
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1       MEVKVENIRGIDMLKARVKNRVARSKCFKNASLVLIGITGLSIALNIYLIINYKMGKNTS 60
99-1       MEVRVENIRAIDMFKAKIKNRIRSSRCYRNATLILIGLTGLSMALNIFLIIDHATTRNVI 60

                    70        80        90       100       110       120
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1       ESEHHTSSSPHESSRETPTVPTDNSDTNSSPCHPTQQSTESGSTLYPAASASSPEHPTST 120
99-1       KTENCAMPSEPSKKTPMTSTAGHNTKPNPCQTCWTTENSTSPVATPEGHPYTGHTQT 120

                   130       140       150       160       170       180
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1       EDTTNRPPFVQHTTPPSASRTKTSPAVHTKNNEPTSSRTHSPPRATTRTARPTTTRTS 180
99-1       SDTTAPQQTTQKHTAPLKSTNEQHTQTTTEPKTIRATTQKRBKGKENTNQTTSDAATQTT 180

                   190       200       210       220       230
           ....|....|....|....|....|....|....|....|....|....|....|
00-1       STEKRPSTASVQPDISATTHKNEPASPASEQTSASTTEQRTSVEANTSTTYNQTS 236
99-1       NTTNQHRNASBT-----TPTSQRPRTDTTTQSSEQTTPATDPSSPPHTA------ 224
```

FIGURE 50

N-terminus of polymerase protein (L)

```
              10        20        30        40        50        60
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MDPLESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRL 60
99-1  MDPFCESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAVENPVVEHVRL 60

              70        80        90       100       110       120
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  KNAVNSKMKISDYKIVEPVNMQHEIMKNVHSCELTLLKQFLTRSKNISTLKLNMICDWLQ 120
99-1  RNAVVTKMKISDYKVVEPVNMQHEIMKNIHSCELTLLKQFLTRSKNISSLKLNMICDWLQ 120

             130       140       150       160       170       180
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LKSTSDDTSILSFIDVEFIPSWVSNWFSNWYNLNKLILEFRKEEVIRTGSILCRSLGKLV 180
99-1  LKSTSDNTSILNFIDVEFIPWWVSNWFSNWYNLNKLILEFRREEVIRTGSILCRSLGKLV 180

             190       200       210       220       230       240
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  FVVSSYGCIVKSNKSKRVSFFTYNQLLTWKDVMLSRFNANFCIWVSNSLNENQEGLGLRS 240
99-1  FIVSSYGCVVKSNKSKRVSFFTYNQLLTWKDVMLSRFNANFCIWVSNNLNKNQEGLGLRS 240

             250       260       270       280       290       300
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  NLQGILTNKLYETVDYMLSLCCNEGFSLVKBFEGFIMSEILRITEHAQFSTRFRNTLLNG 300
99-1  NLQGMLTNKLYETVDYMLSLCCNEGFSLVKBFEGFIMSEILKITEHAQFSTRFRNTLLNG 300

             310       320       330       340       350       360
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LTDQLTKLNKNRDRVEGTVLENNDYPMYEVVLKLLGDTLRGIKLLINKNLENAAELYYI 360
99-1  LTEQLSVLKAKNRSRVLGTILENNNYPMYEVVLKLLGDTLKSIKLLINKNLENAAELYYI 360

             370       380       390       400       410       420
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  FRIFGHPMVDERDAMDAVKLNNEITKILRMESLTELRGAFILRIIKGFVDNNKRWPKIKN 420
99-1  FRIFGHPMVDEREAMDAVKLNNEITKILRLESLTELRGAFILRIIKGFVDNNKRWPKIKN 420

             430       440       450       460       470       480
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LKVLSKRWAMYFKAKSYPSQLELSPQDFLELAAIQFEQEFSVPEKTNLEMVLNDKAISPP 480
99-1  LKVLSKRWAMYFKAKSYPSQLELSVQDFLELAAVQFEQEFSVPEKTNLEMVLNDKAISPP 480

             490
      ....|....|....|....|
00-1  KRLIWSVYPKNYLPEKIKN 499
99-1  KKLIWSVYPKNYLPETIKN 499
```

FIGURE 51

A

Pos., ORF Stop		Non-coding sequence	Gene start	Start Pos., ORF
1, Le		ACGCAGAAAAAAACCCGGUUAUAAUUUAGAUUCCUAAAAAAAUU.................	GGGACAAGUGAAA AUG	55, N
1237, N	UAA	UUUAUAAAGU.................	GGGACAACGUCAAA AUG	1263, P
2145, P	UAG	UUUAAUUAAAUAACAUU.................	GGGACAAGUAAA AUG	2180, M
2942, M	UAA	CAACCAGCACCUUGGCCAAGACGCUACUUAACCCUUUCUCUAUAGUCUCUUAUAGUUCUUAAAGUCCACCAUUCUAGUAUAU AAUAUUUCAAGUUAGCAACAGAUUUAAUCCAUCAGUAC.................	GGGACAAUUAAA AUG	3067, F
4684, F	UAG	UUUAUUUAAAUUAAAGGUAAAAUUAAUAAUUAAAAUUAAAUUAAAAAUUU.................	GGGCCAAUUCUUA AUG	4752, M2
5476, M2	UAG	UAAUUUAAUCACUCAGAGU.................	GGGACAAUUGACA AUG	5509, SH
6058, SH	UAA	AUGUUAACACCAGUUAUCGAUCCUAUCCAAGUUGUUAGUCAACAAUUUUAUAAGUUUUAUUUUAAAAAUUAUUGA AAACAGUAGACUCUAUAUCGGAUCUUCUAUAAUAUAGAUUAAUAUUUAGUUCUUAUAACUCUCACAUACAU UAUUCGAAACUAUUAUUCAUUUAAAAGUUAAAACACACGAACACAU.................	GGGACCAAGUAGU AUG	6262, G
6910, G	UAA	CAAAAUAUUACAAAUAACUCUAGUAUAACCAAUCAAGUUCCAAGAUCCCAAGUCAGAUCAUCCAAAGACAAUUUCA CAAAUUCUCCAAAAAGCAUAUCACAACAUUUGAUUGGUAAGCUGCCAAUUGUGUACUCGUCGGCCCA UUUACAAAUCACAACAUCCCACCCCAAGAAAAAAUCGGGUAAACACACACCCCA.................	GAGACCAAUUACA AUG	7182, L
13197, L	UGA	AAAAUGAUGAAAAUUGAUUUAAACAGGGCAUCAAUUCAUCUAUUCCUAAAGAUAUCUUGAUUUAAAACGAAUU AUGUUAUAUCUAAAUAAAUAUAUUUAAUUUAAGUUAAACAUAUACACUGUCAUGUAUAAGUAUAUAAAUA UAAGAAAUUAUAUUGUGAUUUUGUDAUACGCGGUUUUUUCUCGU		13376, Tr

	1 10	. . . . .	 30
00-1 1-9000	- - - - - - - - - -	- - - - -	G T A T A A A T T A G A T T C
99-1 1-9000	A C G C G A A A A A	A A C G C G T A T A	A A T T A A A T T C

	 40	 50	 60
00-1 1-9000	C A A A A A A T A	T G G G A C A A G T	G A A A A T G T C T
99-1 1-9000	C A A A C A A A - A	C G G G A C A A A T	A A A A A T G T C T

	 70	 80	 90
00-1 1-9000	C T T C A A G G G A	T T C A C C T G A G	T G A T T T A T C A
99-1 1-9000	C T T C A A G G G A	T T C A C C T A A G	T G A T C T A T C A

	 100	 110	 120
00-1 1-9000	T A C A A G C A T G	C T A T A T T A A A	A G A G T C T C A G
99-1 1-9000	T A T A A A C A T G	C T A T A T T A A A	A G A G T C T C A G

	 130	 140	 150
00-1 1-9000	T A C A C A A T A A	A A A G A G A T G T	G G G T A C A A C A
99-1 1-9000	T A C A C A A T A A	A A A G A G A T G T	A G G C A C C A C A

	 160	 170	 180
00-1 1-9000	A C T G C A G T G A	C A C C C T C A T C	A T T G C A A C A A
99-1 1-9000	A C T G C A G T G A	C A C C T T C A T C	A T T A C A A C A A

	 190	 200	 210
00-1 1-9000	G A A A T A A C A C	T G T T G T G T G G	A G A A A T T C T G
99-1 1-9000	G A A A T A A C A C	T T T T G T G T G G	G G A A A T A C T T

	 220	 230	 240
00-1 1-9000	T A T G C T A A A C	A T G C T G A C T A	C A A A T A T G C T
99-1 1-9000	T A C A C T A A A C	A C A C T G A T T A	C A A A T A T G C T

	 250	 260	 270
00-1 1-9000	G C A G A A A T A G	G A A T A C A A T A	T A T T A G C A C A
99-1 1-9000	G C T G A G A T A G	G A A T A C A A T A	T A T T T G C A C A

	 280	 290	 300
00-1 1-9000	G C T T T A G G A T	C A G A G A G A G T	G C A G C A G A T T
99-1 1-9000	G C T C T A G G A T	C A G A A A G A G T	A C A C A G A T T

	 310	 320	 330
00-1 1-9000	C T G A G G A A C T	C A G G C A G T G A	A G T C C A A G T G
99-1 1-9000	T T G A G A A A C T	C A G G T A G T G A	A G T T C A G G T G

	 340	 350	 360
00-1 1-9000	G T C T T A A C C A	G A A C G T A C T C	T C T G G G A A A
99-1 1-9000	G T T C T A A C C A	A A A C A T A C T C	C T T A G G G A A A

	 370	 380	 390
00-1 1-9000	A T T A A A A A C A	A T A A A G G A G A	A G A T T T A C A G
99-1 1-9000	G G C A A A A A C A	G T A A A G G G G A	A G A G C T G C A G

Figure 53

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                         . . . . 400          . . . .              . . . .      420
00-11-9000  A T G T T A G A C A   T A C A C G G G G T   A G A G A A G A G C
99-11-9000  A T G T T A G A T A   T A C A T G G A G T   G G A A A A G A G T

                         . . . . 430          . . . . 440          . . . . 450
00-11-9000  T G G G T A G A A G   A G A T A G A C A A   A G A A G C A A G G
99-11-9000  T G G A T A G A A G   A A A T A G A C A A   A G A G G C A A G A

                         . . . . 460          . . . . 470          . . . . 480
00-11-9000  A A A A C A A T G G   C A A C C T T G C T   T A A G G A A T C A
99-11-9000  A A G A C A A T G G   T A A C T T T G C T   T A A G G A A T C A

                         . . . . 490          . . . . 500          . . . . 510
00-11-9000  T C A G G T A A T A   T C C C A C A A A A   T C A G A G G C C C
99-11-9000  T C A G G T A A C A   T C C C A C A A A A   C C A G A G A C C T

                         . . . . 520          . . . . 530          . . . . 540
00-11-9000  T C A G C A C C A G   A C A C A C C C A T   A A T C T T A T T A
99-11-9000  T C A G C A C C A G   A C A C A C C A A T   A A T T T T A T T A

                         . . . . 550          . . . . 560          . . . . 570
00-11-9000  T G T G T A G G T G   C C T T A A T A T T   C A C T A A A C T A
99-11-9000  T G T G T A G G T G   C C C T A A T A T T   C A C T A A A C T A

                         . . . . 580          . . . . 590          . . . . 600
00-11-9000  G C A T C A A C C A   T A G A A G T G G G   A C T A G A G A C C
99-11-9000  G C A T C A A C C A   T A G A A G T T G G   A T T A G A G A C T

                         . . . . 610          . . . . 620          . . . . 630
00-11-9000  A C A G T C A G A A   G G G C T A A C C G   T G T A C T A A G T
99-11-9000  A C A G T T A G A A   G A G C T A A T A G   A G T G C T A A G T

                         . . . . 640          . . . . 650          . . . . 660
00-11-9000  G A T G C A C T C A   A G A G A T A C C C   T A G A A T G G A C
99-11-9000  G A T G C A C T C A   A A A G A T A C C C   A A G G A T A G A T

                         . . . . 670          . . . . 680          . . . . 690
00-11-9000  A T A C C A A A G A   T T G C C A G A T C   C T T C T A T G A C
99-11-9000  A T A C C A A A G A   T T G C T A G A T C   T T T T T A T G A A

                         . . . . 700          . . . . 710          . . . . 720
00-11-9000  T T A T T T G A A C   A A A A A G T G T A   T C A C A G A A G T
99-11-9000  C T A T T T G A A C   A A A A A G T G T A   C T A C A G A A G T

                         . . . . 730          . . . . 740          . . . . 750
00-11-9000  T T G T T C A T T G   A G T A T G G C A A   A G C A T T A G G C
99-11-9000  T T A T T C A T T G   A G T A C G G C A A   A G C T T T A G G C

                         . . . . 760          . . . . 770          . . . . 780
00-11-9000  T C A T C A T C T A   C A G G C A G C A A   A G C A G A A A G T
99-11-9000  T C A T C T T C A A   C A G G A A G C A A   A G C A G A A A G T
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Figure 53 cont'd

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                             790                    800                    810
00-11-9000   C T A T T T G T T A   A T A T A T T C A T   G C A A G C T T A T
99-11-9000   T T G T T T G T A A   A T A T A T T T A T   G C A A G C T T A T

                             820                    830                    840
00-11-9000   G G G G C C G G T C   A A A C A A T G C T   A A G G T G G G G G
99-11-9000   G G A G C T G G C C   A A A C A C T G C T   A A G G T G G G G T

                             850                    860                    870
00-11-9000   G T C A T T G C C A   G G T C A T C C A A   C A A T A T A A T G
99-11-9000   G T C A T T G C C A   G A T C A T C C A A   C A A C A T A A T G

                             880                    890                    900
00-11-9000   T T A G G A C A T G   T A T C C G T C C A   A G C T G A G T T A
99-11-9000   C T A G G C A T G   T A T C T G T G C A   A T C T G A A T T G

                             910                    920                    930
00-11-9000   A A A C A G G T C A   C A G A G T C T A   T G A C T T G G T G
99-11-9000   A A G C A A G T T A   C A G A G G T T T A   T G A C T T G G T G

                             940                    950                    960
00-11-9000   C G A G A A A T G G   G C C C T G A A T C   T G G A C T T C T A
99-11-9000   A G A G A A A T G G   G T C C T G A A T C   T G G G C T T T T A

                             970                    980                    990
00-11-9000   C A T T T A A G G C   A A A G C C C A A A   A G C T G G A C T G
99-11-9000   C A T C T A A G A C   A A A G T C C A A A   G G C A G G G C T G

                            1000                   1010                   1020
00-11-9000   T T A T C A C T A G   C C A A C T G T C C   C A A C T T T G C A
99-11-9000   T T A T C A T T G G   C C A A T T G C C C   C A A T T T T G C T

                            1030                   1040                   1050
00-11-9000   A G T G T T G T T C   T C G G A A A T G C   C T C A G G C T T A
99-11-9000   A G T G T T G T T C   T T G G C A A T G C   T T C A G G T C T A

                            1060                   1070                   1080
00-11-9000   G G C A T A A T C G   G T A T G T A T C G   A G G G A G A G T A
99-11-9000   G G C A T A A T C G   G A A T G T A C A G   A G G G A G A G T A

                            1090                   1100                   1110
00-11-9000   C C A A A C A C A G   A A T T A T T T C   A G C A G C T G A A
99-11-9000   C C A A A C A C A G   A G C T A T T T T C   T G C A G C A G A A

                            1120                   1130                   1140
00-11-9000   A G T T A T G C C A   A A A G T T T G A A   A G A A A G C A A T
99-11-9000   A G T T A T G C C A   G A A G C T T A A A   A G A A A G C A A T

                            1150                   1160                   1170
00-11-9000   A A A A T A A A T T   T C T C T T C A T T   A G G A C T T A C A
99-11-9000   A A A A T C A A C T   T C T C T T C G T T   A G G G C T T A C A
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Figure 53 cont'd

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                              1180                    1190                    1200
00-11-9000  G A T G A A G A G A    A A G A G G C T G C    A G A A C A T T T C
99-11-9000  G A T G A A G A A A    A A G A A G C T G C    A G A A C A C T T C

                              1210                    1220                    1230
00-11-9000  T T A A A T G T G A    G T G A C G A C G A    T C A A A A T G A T
99-11-9000  T T A A A C A T G A    G T G G T G A C A A    T C A A G A T G A T

                              1240                    1250                    1260
00-11-9000  T A T G A G T A A T    T A A A A A A G T G    G G A C A A G T C A
99-11-9000  T A T G A G T A A T    T A A A A A A C T G    G G A C A A G T C A

                              1270                    1280                    1290
00-11-9000  A A A T G T C A T T    C C C T G A A G G A    A A A G A T A T T C
99-11-9000  A A A T G T C A T T    C C C T G A A G G A    A A G G A T A T T C

                              1300                    1310                    1320
00-11-9000  T T T T C A T G G G    T A A T G A A G C A    G C A A A A T T A G
99-11-9000  T G T T C A T G G G    T A A T G A A G C A    G C A A A A A T A G

                              1330                    1340                    1350
00-11-9000  C A G A A G C T T T    C C A G A A A T C A    T T A A G A A A A C
99-11-9000  C C G A A G C T T T    C C A G A A A T C A    C T G A A A A A A T

                              1360                    1370                    1380
00-11-9000  C A G G T C A T A A    A A G A T C T C A A    T C T A T T A T A G
99-11-9000  C A G G T C A C A A    G A G A A C T C A A    T C T A T T G T A G

                              1390                    1400                    1410
00-11-9000  G A G A A A A A G T    G A A T A C T G T A    T C A G A A A C A T
99-11-9000  G G G A A A A A G T    T A A C A C T A T A    T C A G A A A C T C

                              1420                    1430                    1440
00-11-9000  T G G A A T T A C C    T A C T A T C A G T    A G A C C T G C A A
99-11-9000  T A G A A C T A C C    T A C C A T C A G C    A A A C C T G C A C

                              1450                    1460                    1470
00-11-9000  A A C C A A C C A T    A C C G T C A G A A    C C A A A G T T A G
99-11-9000  G A T C A T C T A C    A C T G C T G G A A    C C A A A A T T G G

                              1480                    1490                    1500
00-11-9000  C A T G G A C A G A    T A A A G G T G G G    G C A A C C A A A A
99-11-9000  C A T G G G C A G A    C A A C A G C G G A    A T C A C C A A A A

                              1510                    1520                    1530
00-11-9000  C T G A A A T A A A    G C A A G C A A T C    A A A G T C A T G G
99-11-9000  T C A C A G A A A A    A C C A G C A A C C    A A A A C A A C A G

                              1540                    1550                    1560
00-11-9000  A T C C A T T G A    A G A A G A A G A G    T C T A C C G A G A
99-11-9000  A T C C T G T T G A    A G A A G A G G A A    T T C A A T G A A A
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Figure 53 cont'd

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                              1570                1580                1590
00-1 1-9000  A G A A G G T G C T   A C C C T C C A G T   G A T G G G A A A A
99-1 1-9000  A G A A A G T G T T   A C C T T C C A G T   G A T G G G A A G A

                              1600                1610                1620
00-1 1-9000  C C C C T G C A G A   A A A G A A A C T G   A A A C C A T C A A
99-1 1-9000  C T C C T G C A G A   G A A A A A A T C A   A A G T T T T C A A

                              1630                1640                1650
00-1 1-9000  C T A A C A C C A A   A A A G A A A G T T   T C A T T T A C A C
99-1 1-9000  C C A G T G T A A A   A A A G A A A G T T   T C C T T T A C A T

                              1660                1670                1680
00-1 1-9000  C A A A T G A A C C   A G G G A A A T A T   A C A A A G T T G G
99-1 1-9000  C A A A T G A A C C   A G G G A A A T A C   A C C A A A C T A G

                              1690                1700                1710
00-1 1-9000  A A A A A G A T G C   T C T A G A T T T G   C T C T C A G A T A
99-1 1-9000  A G A A A G A T G C   C C T A G A T T T G   C T C T C A G A C A

                              1720                1730                1740
00-1 1-9000  A T G A A G A A G A   A G A T G C A G A A   T C T T C A A T C T
99-1 1-9000  A T G A G G A A G A   A G A C G C A G A A   T C C T C A A T C C

                              1750                1760                1770
00-1 1-9000  T A A C C T T T G A   A G A A A G A G A T   A C T T C A T C A T
99-1 1-9000  T A A C T T T T G A   G G A G A A A G A T   A C A T C A T C A C

                              1780                1790                1800
00-1 1-9000  T A A G C A T T G A   G G C C A G A T T G   G A A T C A A T A G
99-1 1-9000  T A A G C A T T G A   A G C T A G A C T A   G A A T C T A T A G

                              1810                1820                1830
00-1 1-9000  A G G A G A A A T T   A A G C A T G A T A   T T A G G G C T A T
99-1 1-9000  A A G A G A A G T T   G A G C A T G A T A   T T A G G A C T G C

                              1840                1850                1860
00-1 1-9000  T A A G A A C A C T   C A A C A T T G C T   A C A G C A G G A C
99-1 1-9000  T T C G T A C A C T   T A A C A T T G C A   A C A G C A G G A C

                              1870                1880                1890
00-1 1-9000  C C A C A G C A G C   A A G A G A T G G G   A T C A G A G A T G
99-1 1-9000  C A A C A G C T G C   A C G A G A T G G A   A T T A G G G A T G

                              1900                1910                1920
00-1 1-9000  C A A T G A T T G G   C G T A A G A G A G   G A A T T A A T A G
99-1 1-9000  C A A T G A T T G G   T A T A A G A G A A   G A G C T A A T A G

                              1930                1940                1950
00-1 1-9000  C A G A C A T A A T   A A A G G A A G C T   A A A G G G A A A G
99-1 1-9000  C A G A C A T A A T   T A A G G A A G C C   A A G G G A A A G
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Figure 53 cont'd

Figure 53 cont'd

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                          2350                2360              2370
00-1 1-9000  C C T G A C A A T A    A C C A C T C T G T    A T G C T G C A T C
99-1 1-9000  C C T G A C A A T A    A C C A C T C T G T    A T G C T G C A T C

                          2380                2390              2400
00-1 1-9000  A C A A A A T G G T    C C A A T A C T C A    A A G T G A A T G C
99-1 1-9000  A C A G A A T G G T    C C A A T A C T C A    A G G T A A A T G C

                          2410                2420              2430
00-1 1-9000  A T C A G C C C A A    G G T G C A G C A A    T G T C T G T A C T
99-1 1-9000  A T C T G C C C A A    G G T G C T G C C A    T G T C T G T A C T

                          2440                2450              2460
00-1 1-9000  T C C C A A A A A A    T T T G A A G T C A    A T G C G A C T G T
99-1 1-9000  T C C C A A A A A A    T T C G A G G T A A    A T G C G A C T G T

                          2470                2480              2490
00-1 1-9000  A G C A C T C G A T    G A A T A T A G C A    A A C T G G A A T T
99-1 1-9000  A G C A C T G A T    G A A T A C A G T A    A A C T T G A T T T

                          2500                2510              2520
00-1 1-9000  T G A C A A A C T C    A C A G T C T G T G    A A G T A A A A A C
99-1 1-9000  T G A C A A G C T G    A C G G T C T G C G    A T G T T A A A A C

                          2530                2540              2550
00-1 1-9000  A G T T T A C T T A    A C A A C C A T G A    A A C C A T A C G G
99-1 1-9000  A G T T T A T T T G    A C A A C C A T G A    A A C C G T A C G G

                          2560                2570              2580
00-1 1-9000  G A T G G T A T C A    A A A T T T G T G A    G C T C A G C C A A
99-1 1-9000  G A T G G T G T C A    A A A T T T G T G A    G T T C A G C C A A

                          2590                2600              2610
00-1 1-9000  A T C A G T T G G C    A A A A A A A C A C    A T G A T C T A A T
99-1 1-9000  A T C A G T T G G C    A A A A A G A C A C    A T G A T C T A A T

                          2620                2630              2640
00-1 1-9000  C G C A C T A T G T    G A T T T T A T G G    A T C T A G A A A A
99-1 1-9000  T G C A C T A T G T    G A C T T C A T G G    A C C T A G A G A A

                          2650                2660              2670
00-1 1-9000  G A A C A C A C C T    G T T A C A A T A C    C A G C A T T C A T
99-1 1-9000  A A A T A T A C C T    G T G A C A A T A C    C A G C A T T C A T

                          2680                2690              2700
00-1 1-9000  C A A A T C A G T T    T C A A T C A A A C    A G A G T G A G T C
99-1 1-9000  A A A G T C A G T T    T C A A T C A A A G    A G A G T G A A T C

                          2710                2720              2730
00-1 1-9000  A G C T A C T G T T    G A A G C T G C T A    T A A G C A G T G A
99-1 1-9000  A G C C A C T G T T    G A A G C T G C A A    T A A G C A G C G A
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Figure 53 cont'd

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                                                          2760
00-1 1-9000  A G C A G A C C A A   G C T C T A A C A C   A G G C C A A A A T
99-1 1-9000  A G C C G A C C A A   G C C T T G A C A C   A A G C C A A G A T

                     2770                 2780                 2790
00-1 1-9000  T G C A C C T T A T   G C G G G A T T A A   T T A T G A T C A T
99-1 1-9000  T G C G C C T A T     G C A G G A C T A A   T T A T G A T C A T

                     2800                 2810                 2820
00-1 1-9000  G A C T A T G A A C   A A T C C C A A A G   G C A T A T T C A A
99-1 1-9000  G A C C A T G A A C   A A T C A C A A A G   G T A T A T T C A A

                     2830                 2840                 2850
00-1 1-9000  A A A G C T T G G A   G C T G G G A C T C   A A G T C A T A G T
99-1 1-9000  G A A C T A G G G     G C T G G A A C A C   A A G T G A T A G T

                     2860                 2870                 2880
00-1 1-9000  A G A A C T A G G A   G C A T A T G T C C   A G G C T G A A A G
99-1 1-9000  A G A G C T G G G G   G C A T A T G T T C   A G G C T G A G A G

                     2890                 2900                 2910
00-1 1-9000  C A T A A G C A A A   A T A T G C A A G A   C T T G G A G C C A
99-1 1-9000  C A T C A G T A G G   A T C T G C A A G A   G C T G G A G T C A

                     2920                 2930                 2940
00-1 1-9000  T C A A G G A A C A   A G A T A T G T C T   T G A A G T C C A G
99-1 1-9000  C C A A G G A A C A   A G A T A C G T A C   T A A A A T C C A G

                     2950                 2960                 2970
00-1 1-9000  A T A A C A A C C A   A G C A C C T T G G   C C A A G A G C T A
99-1 1-9000  A T A A - A A A T A   A C T G T C T T A A   T C A A T A A T T G

                     2980                 2990                 3000
00-1 1-9000  C T A A C C C T A T   C T C A T A G A T C   A - T A A A G T C A
99-1 1-9000  C T T A T A T A A C   T C T A G A G A T T   A A T A A G C T T A

                     3010                 3020                 3030
00-1 1-9000  C C A T T C T A G T   T A T A T A A A A A   T C A A G T T A G A
99-1 1-9000  T T A T T A T A G T   T A T A T A A A A T   T - A A A T T A G A

                     3040                 3050                 3060
00-1 1-9000  A C A A G A A T T A   A A T C A A T C A A   G A A C G G G A C A
99-1 1-9000  A T T A G A A G G G   C A T C A A T A G A   A A G C G G G A C A

                     3070                 3080                 3090
00-1 1-9000  A A T A A A A A T G   T C T T G G A A A G   T G G T G A T C A T
99-1 1-9000  A A T A A A A A T G   T C T T G G A A A G   T G A T G A T C A T

                     3100                 3110                 3120
00-1 1-9000  T T T T T C A T T G   T T A A T A A C A C   C T C A A C A C G G
99-1 1-9000  C A T T T C G T T A   C T C A T A A C A C   C C C A G C A C G G
```

Figure 53 cont'd

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	3130	3140	3150
00-11-9000	T C T T A A A G A G	A G C T A C T T A G	A A G A G T C A T G
99-11-9000	G C T A A A G G A G	A G T T A T T T G G	A A G A A T C A T G

	3160	3170	3180
00-11-9000	T A G C A C T A T A	A C T G A A G G A T	A T C T C A G T G T
99-11-9000	T A G T A C T A T A	A C T G A G G G A T	A C C T C A G T G T

	3190	3200	3210
00-11-9000	T C T G A G G A C A	G G T T G G T A C A	C C A A T G T T T T
99-11-9000	T T T A A G A A C A	G G C T G G T A C A	C T A A T G T C T T

	3220	3230	3240
00-11-9000	T A C A C T G G A G	G T A G G C G A T G	T A G A G A A C C T
99-11-9000	C A C A T T A G A A	G T T G G T G A T G	T T G A A A A T C C

	3250	3260	3270
00-11-9000	T A C A T G T G C C	G A T G G A C C C A	G C T T A A T A A A
99-11-9000	T A C A T G T A C T	G A T G G A C C T A	G C T T A A T C A A

	3280	3290	3300
00-11-9000	A A C A G A A T T A	G A C C T G A C C A	A A A G T G C A C T
99-11-9000	A A C A G A A C T T	G A T C T A A C A A	A A A G T G C T T T

	3310	3320	3330
00-11-9000	A A G A G A G C T C	A G A A C A G T T T	C T G C T G A T C A
99-11-9000	A A G A G A G C T C	A A A A C A G T C T	C T G C T G A T C A

	3340	3350	3360
00-11-9000	A C T G G C A G A A	G A G G A G C A A A	T T G A A A A T C C
99-11-9000	G T T G G C G A G A	G A G G A G C A A A	T T G A A A A T C C

	3370	3380	3390
00-11-9000	C A G A C A A T C T	A G A T T C G T T C	T A G G A G C A A T
99-11-9000	C A G A C A A T C A	A G A T T T G T C T	T A G G T G C A T

	3400	3410	3420
00-11-9000	A G C A C T C G G T	G T T G C A A C T G	C A G C T G C A G T
99-11-9000	A G C T C T C G G A	G T T G C T A C A G	C A G C A G C A G T

	3430	3440	3450
00-11-9000	T A C A G C A G G T	G T T G C A A T T G	C C A A A A C C A T
99-11-9000	C A C A G C A G G C	A T T G C A A A T A G	C C A A A A C C A T

	3460	3470	3480
00-11-9000	C C G G C T T G A A	A G T G A A G T A A	C A G C A A T T A A
99-11-9000	A A G G C T T G A G	A G T G A G G T G A	A T G C A A T T A A

	3490	3500	3510
00-11-9000	G A A T G C C C T C	A A A A A G A C C A	A T G A A G C A G T
99-11-9000	A G G T G C T C T C	A A A C A A A C T A	A T G A A G C A G T

Figure 53 cont'd

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                    . 3520  .    .  .   . 3530  .              . 3540
00-1 1-9000 A T C T A C A T T G  G G G A A T G G A G  T T C G T G T G T T
99-1 1-9000 A T C C A C A T T A  G G G A A T G G T G  T G C G G G T C C T

                    . 3550  .    .  .   . 3560  .              . 3570
00-1 1-9000 G G C A A C T G C A  G T G A G A G A G C  T G A A A G A T T T
99-1 1-9000 A G C C A C T G C A  G T G A G A G A G C  T A A A A G A T T T

                    . 3580  .    .  .   . 3590  .              . 3600
00-1 1-9000 T G T G A G C A A G  A A T C T A A C A C  G T G C A A T C A A
99-1 1-9000 T G T G A G C A A A  A A C C T G A C T A  G T G C A A T C A A

                    . 3610  .    .  .   . 3620  .              . 3630
00-1 1-9000 C A A A A C A A G  T G C G A C A T T G  C T G A C C T G A A
99-1 1-9000 C A G G A A C A A A  T G T G A C A T T G  C T G A T C T G A A

                    . 3640  .    .  .   . 3650  .              . 3660
00-1 1-9000 A A T G G C C G T T  A G C T T C A G T C  A A T T C A A C A G
99-1 1-9000 G A T G G C T G T C  A G C T T C A G T C  A A T T C A A C A G

                    . 3670  .    .  .   . 3680  .              . 3690
00-1 1-9000 A A G G T T C C T A  A A T G T T G T G C  G G C A A T T T T C
99-1 1-9000 A A G A T T T C T A  A A T G T T G T G C  G G C A G T T T T C

                    . 3700  .    .  .   . 3710  .              . 3720
00-1 1-9000 A G A C A A C G C T  G G A A T A A C A C  C A G C A A T A T C
99-1 1-9000 A G A C A A T G C A  G G A A T A A C A C  C A G C A A T A T C

                    . 3730  .    .  .   . 3740  .              . 3750
00-1 1-9000 T T T G G A C T T A  A T G A C A G A T G  C T G A A C T A G C
99-1 1-9000 A T T G G A C C T G  A T G A C T G A T G  C T G A G T T G G C

                    . 3760  .    .  .   . 3770  .              . 3780
00-1 1-9000 C A G A G C T G T T  T C C A A C A T G C  C A A C A T C T G C
99-1 1-9000 C A G A G C T G T A  T C A T A C A T G C  C A A C A T C T G C

                    . 3790  .    .  .   . 3800  .              . 3810
00-1 1-9000 A G G A C A A A T A  A A A C T G A T G T  T G G A G A A C C G
99-1 1-9000 A G G G C A G A T A  A A A C T G A T G T  T G G A G A A C C G

                    . 3820  .    .  .   . 3830  .              . 3840
00-1 1-9000 T G C A A T G G T A  A G A A G A A A A G  G G T T C G G A T T
99-1 1-9000 C G C A A T G G T A  A G G A G A A A A G  G A T T T G G A A T

                    . 3850  .    .  .   . 3860  .              . 3870
00-1 1-9000 C C T G A T A G G A  G T T T A C G G A A  G C T C C G T A A T
99-1 1-9000 C C T G A T A G G G  G T C T A C G G A A  G C T C T G T G A T

                    . 3880  .    .  .   . 3890  .              . 3900
00-1 1-9000 T T A C A T G G T G  C A A C T G C C A A  T C T T T G G G G T
99-1 1-9000 T T A C A T G G T T  C A A T T G G T G T  T C T T T G G T G T
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Figure 53 cont'd

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                     3910                    3920                    3930
00-11-9000  T A T A G A C A C G    C C T T G C T G G A    T A G T A A A A G C
99-11-9000  C A T A G A T A C A    C C T T G T T G G A    T C A T C A A G G C

                     3940                    3950                    3960
00-11-9000  A G C C C C T T C T    T G T T C A G G A A    A A A A G G G A A A
99-11-9000  A G C T C C C T C T    T G C T C A G A A A    A A A A C G G G A A

                     3970                    3980                    3990
00-11-9000  C T A T G C T T G C    C T C T T A A G A G    A A G A C C A A G G
99-11-9000  T T A T G C T T G C    C T C C T A A G A G    A G G A T C A A G G

                     4000                    4010                    4020
00-11-9000  A T G G T A T T G T    C A A A A T G C A G    G G T C A A C T G T
99-11-9000  G T G G T A T T G T    A A A A A T G C A G    G A T C A A C T G T

                     4030                    4040                    4050
00-11-9000  T T A C T A C C C A    A A T G A A A A G C    A C T G T G A A A C
99-11-9000  T T A C T A C C C A    A A T G A A A A A G    A C T G C G A A A C

                     4060                    4070                    4080
00-11-9000  A A G A G G A G A C    C A T G T C T T T T    G C G A C A C A G C
99-11-9000  A A G A G G T G A T    C A T G T T T T T T    G T G A C A C A G C

                     4090                    4100                    4110
00-11-9000  A G C A G G A A T C    A A T G T T G C T G    A G C A G T C A A A
99-11-9000  A G C A G G G A T C    A A T G T T G C T G    A G C A A T C A A G

                     4120                    4130                    4140
00-11-9000  G G A G T G C A A C    A T A A A C A T A T    C T A C T A C T A A
99-11-9000  A G A A T G C A A C    A T C A A C A T A T    C T A C T A C C A A

                     4150                    4160                    4170
00-11-9000  T T A C C C A T G C    A A A G T T A G C A    C A G G A A G A C A
99-11-9000  C T A C C C A T G C    A A A G T C A G C A    C A G G A A G A C A

                     4180                    4190                    4200
00-11-9000  T C C T A T C A G T    A T G G T T G C A C    T A T C T C C T C T
99-11-9000  C C C T A T A A G C    A T G G T T G C A C    T A T C A C C T C T

                     4210                    4220                    4230
00-11-9000  T G G G G C T T T G    G T T G C T T G C T    A C A A G G G A G T
99-11-9000  C G G T G C T T T G    G T G G C T T G C T    A T A A A G G G G T

                     4240                    4250                    4260
00-11-9000  G A G C T G T T C C    A T T G G C A G C A    A C A G A G T A G G
99-11-9000  A A G C T G C T C G    A T T G G C A G C A    A T T G G G T T G G

                     4270                    4280                    4290
00-11-9000  G A T C A T C A A G    C A A C T G A A C A    A A G G C T G C T C
99-11-9000  A A T C A T C A A A    C A A T T A C C C A    A A G G C T G C T C
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Figure 53 cont'd

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                    .    .    .   4300  .    .    .    .   4310  .    .    .  .   4320
00-11-9000  T T A T A T A A C C   A A C C A A G A C G   C A G A C A C A G T
99-11-9000  A T A C A T A A C C   A A C C A G G A T G   C A G A C A C T G T

                    .    .    .   4330  .    .    .    .   4340  .    .    .    .   4350
00-11-9000  G A C A A T A G A C   A A C A C T G T A T   A C C A G C T A A G
99-11-9000  A A C A A T T G A C   A A T A C C G T G T   A T C A A C T A A G

                    .    .    .   4360  .    .    .    .   4370  .    .    .    .   4380
00-11-9000  C A A A G T T G A A   G G C G A A C A G C   A T G T T A T A A A
99-11-9000  C A A A G T T G A A   G G T G A A C A G C   A T G T A A T A A A

                    .    .    .   4390  .    .    .    .   4400  .    .    .    .   4410
00-11-9000  A G G A A G G C C A   G T G T C A A G C A   G C T T T G A C C C
99-11-9000  A G G G A G G A C C A G T T T C A A G C A   G T T T T G A T C C

                    .    .    .   4420  .    .    .    .   4430  .    .    .    .   4440
00-11-9000  A G T C A A G T T T   C C T G A A G A T C   A A T T C A A T G T
99-11-9000  A A T C A A G T T T   C C T G A G G A T C   A G T T C A A T G T

                    .    .    .   4450  .    .    .    .   4460  .    .    .    .   4470
00-11-9000  T G C A C T T G A C   C A A G T T T T C G   A G A G C A T T G A
99-11-9000  T G C G C T T G A T   C A A G T C T T C G   A A A G C A T T G A

                    .    .    .   4480  .    .    .    .   4490  .    .    .    .   4500
00-11-9000  G A A C A G T C A G   G C C T T G G T G G   A T C A A T C A A A
99-11-9000  G A A C A G T C A G   G C A C T A G T G G   A C C A G T C A A A

                    .    .    .   4510  .    .    .    .   4520  .    .    .    .   4530
00-11-9000  C A G A A T C C T A   A G C A G T G C A G   A G A A A G G A A A
99-11-9000  C A A A A T T C T A   A A C A G T G C A G   A A A A A G G A A A

                    .    .    .   4540  .    .    .    .   4550  .    .    .    .   4560
00-11-9000  C A C T G G C T T C   A T C A T T G T A A   T A A T T C T A A T
99-11-9000  C A C T G G T T T C   A T T A T C G T A A   T A A T T T T G G T

                    .    .    .   4570  .    .    .    .   4580  .    .    .    .   4590
00-11-9000  T G C T G T C C T T   G G C T C T A C C A   T G A T C C T A G T
99-11-9000  T G C T G T C T T T   G G T C T A A C C A   T G A T T T C A G T

                    .    .    .   4600  .    .    .    .   4810  .    .    .    .   4620
00-11-9000  G A G T G T T T T T   A T C A T A A T A A   A G A A A C A A A
99-11-9000  G A G C A T C A T C   A T C A T A A T C A   A G A A A A C A A G

                    .    .    .   4630  .    .    .    .   4640  .    .    .    .   4650
00-11-9000  G A A A C C C A C A   G G A G C A C C T C   C A G A G C T G A G
99-11-9000  G A A G C C C A C A   G G A G C A C C T C   C A G A G C C A C A

                    .    .    .   4660  .    .    .    .   4670  .    .    .    .   4680
00-11-9000  T G G T G T C A C A   A A C A A T G G C T   T C A T A C C A C A
99-11-9000  T G G T G T C A C C   A A C G G C G G T T   T C A T A C C A C A
```

Figure 53 cont'd

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                              4690                      4700                      4710
00-11-9000  T A A T T A G T T A    A T T A A A A A T A    A A G T A A A T T A
99-11-9000  T A G T T A G T T A    A T T A A A A A - -    - - - - A - - -

                              4720                      4730                      4740
00-11-9000  A A A T A A A T T A    A A A T T A A A A A    T A A A A T T T G
99-11-9000  - - - - - - - - - -    - - - - - - - - - -    - - - - - - T G

                              4750                      4760                      4770
00-11-9000  G G A C A A A T C A    T A A T G T C T C G    C A A G G C T C C G
99-11-9000  G G A C A A A T C A    T C A T G T C T C G    T A A G G C T C C G

                              4780                      4790                      4800
00-11-9000  T G C A A A T A T G    A A G T G C G G G G    C A A A T G C A A T
99-11-9000  T G C A A A T A T G    A A G T G C G G G G    C A A A T G C A A C

                              4810                      4820                      4830
00-11-9000  A G A G G A A G T G    A G T G C A A G T T    T A A C C A C A A T
99-11-9000  A G A G G G A G T G    A T T G C A A A T T    C A A T C A C A A T

                              4840                      4850                      4860
00-11-9000  T A C T G G A G T T    G G C C A G A T A G    A T A C T T A T T A
99-11-9000  T A C T G G A G T T    G G C C T G A T A - G    A T A T T T A T T G

                              4870                      4880                      4890
00-11-9000  A T A A G A T C A A    A T T A T T T A T T    A A A T C A A C T T
99-11-9000  T T A A G A T C A A    A T T A T C T C T T    A A A T C A G C T T

                              4900                      4910                      4920
00-11-9000  T T A A G G A A C A    C T G A T A G A G C    T G A T G G C T T A
99-11-9000  T T A A G A A A C A    C A G A T A A G G C    T G A T G G T T T G

                              4930                      4940                      4950
00-11-9000  T C A A T A A T A T    C A G G A G C A G G    C A G A G A A G A T
99-11-9000  T C A A T A A T A T    C A G G A G C A G G    T A G A G A A G A T

                              4960                      4970                      4980
00-11-9000  A G G A C A C A A G    A T T T T G T C C T    A G G T T C C A C C
99-11-9000  A G A A C T C A A G    A C T T T G T T C T    T G G T T C T A C T

                              4990                      5000                      5010
00-11-9000  A A T G T G G T T C    A A G G T T A T A T    T G A T G A T A A C
99-11-9000  A A T G T G G T T C    A A G G G T A C A T    T G A T G A C A A C

                              5020                      5030                      5040
00-11-9000  C A A A G C A T A A    A A G G C T G C    A G C C T G T T A C
99-11-9000  C A A G G A A T A A    C C A A G G C T G C    A G C T T G C T A T

                              5050                      5060                      5070
00-11-9000  A G T C A C A T A    A T A T A A T C A A    A C A A C T A C A A
99-11-9000  A G T C T A C A C A    A C A T A A T C A A    G C A A C T A C A A
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Figure 53 cont'd

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                       5080              5090              5100
00-1 1-9000  G A A G T T G A A G   T T A G G C A G G C   T A G A G A T A A C
99-1 1-9000  G A A A C A G A A G   T A A G A C A G G C   T A G A G A C A A C

                       5110              5120              5130
00-1 1-9000  A A A C T A T C T G   A C A G C A A A C A   T G T A G C A C T T
99-1 1-9000  A A G C T T T C T G   A T A G C A A A C A   T G T G G C G C T C

                       5140              5150              5160
00-1 1-9000  C A C A A C T T A G   T C C T A T C T T A   T A T G G A G A T G
99-1 1-9000  C A C A A C T T G A   T A T T A T C C T A   T A T G G A G A T G

                       5170              5180              5190
00-1 1-9000  A G C A A A A C T C   C T G C A T C T T T   A A T C A A C A A T
99-1 1-9000  A G C A A A A C T C   C T G C A T C T C T   A A T C A A C A A C

                       5200              5210              5220
00-1 1-9000  C T C A A G A G A C   T G C C G A G A G A   G A A A C T G A A C
99-1 1-9000  C T A A A G A A A C   T A C C A A G G G A   A A A A C T G A A G

                       5230              5240              5250
00-1 1-9000  A A A T T A G C A A   A G C T C A T A A T   T G A C T T A T C A
99-1 1-9000  A A A T T A G C A A   G A T T A A T A A T   T G A T T T A T C A

                       5260              5270              5280
00-1 1-9000  G C A G G T G C T G   A A A A T G A C T C   T T C A T A T G C C
99-1 1-9000  G C A G G A A C T G   A C A A T G A C T C   T T C A T A T G C C

                       5290              5300              5310
00-1 1-9000  T T G C A A G A C A   G T G A A G C A C   T A A T C A A G T G
99-1 1-9000  T T G C A A G A C A   G T G A A A G C A C   T A A T C A A G T G

                       5320              5330              5340
00-1 1-9000  C A G T G A G C A T   G G T C C A G T T T   T C A T T A C T A T
99-1 1-9000  C A G T A A A C A T   G G T C C C A A A T   T C A T T A C C A T

                       5350              5360              5370
00-1 1-9000  A G A G G T T G A T   G A C A T G A T A T   G G A C T C A C A A
99-1 1-9000  A G A G G C A G A T   G A T A T G A T A T   G G A C T C A C A A

                       5380              5390              5400
00-1 1-9000  G G A C T T A A A A   G A A G C T T T A T   C T G A T G G G A T
99-1 1-9000  A G A A T T A A A A   G A A A C A C T G T   C T G A T G G G A T

                       5410              5420              5430
00-1 1-9000  A G T G A A G T C T   C A T A C T A A C A   T T T A C A A T T G
99-1 1-9000  A G T A A A A T C A   C A C A C C A A T A   T T T A T A G T T G

                       5440              5450              5460
00-1 1-9000  T T A T T T A G A A   A A C A T A G A A A   T T A T A T A T G T
99-1 1-9000  T T A C T T A G A A   A A T A T A G A A A   T A A T A T A T G T
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Figure 53 cont'd

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Figure 53 cont'd

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                    5860              5870              5880
00-1 1-9000  A A A A T A A A C A   G A A A T C A A T G   C A C A A A T A T A
99-1 1-9000  A G A A T A C A C A   A G A A T C A A C G   T A C A A A T A T A

                    5890              5900              5910
00-1 1-9000  A C A A C A T A C A   A A T T T T T A T G   T T T T A A A T C T
99-1 1-9000  A A A A T A T A C A   A G T T C T T A T G   C T C T G G G T T C

                    5920              5930              5940
00-1 1-9000  G A A G A C A C A A   A A A C C A A C A A   T T G T G A T A A A
99-1 1-9000  A C A A A T T C A A   A A G G T A C A G A   T T G T G A G G A A

                    5950              5960              5970
00-1 1-9000  C T G A C A G A T T   T A T G C A G A A A   C A A A C C A A A A
99-1 1-9000  C C A A C A G C C C   T A T G C A G A A A   A A A G T A A A A A

                    5980              5990              6000
00-1 1-9000  C C A G C A G T T G   G A G T G T A T C A   C A T A G T A G A A
99-1 1-9000  A C C A T A G T A G   A A A A A C A T A G   A A A A G C A G A A

                    6010              6020              6030
00-1 1-9000  T G C C A T T G T A   T A T A C A G A A T   T A A A T G G A A G
99-1 1-9000  T G T C A C T G T C   T A C A T A C A A C   C G A G T G G G G G

                    6040              6050              6060
00-1 1-9000  T G C T A T C A T T   A C C C A A C C G A   T G A A A C C C A A
99-1 1-9000  T G C C T T C A T C   C C T A A A A T - -   - - - A A C A C G G

                    6070              6080              6090
00-1 1-9000  T C C T A A A T G T   T A A C A C C G A   T T A G G A T C C A
99-1 1-9000  C T T T C A A C A T   T A A A A T C A G A   A C A A C C T C C A

                    6100              6110              6120
00-1 1-9000  T C C A A G T C T G   T T A G T T C A A C   A A T T T A G T T A
99-1 1-9000  C C C A G G T C T A   T C A A T A C A G T   G G T T T A G C C A

                    6130              6140              6150
00-1 1-9000  T T T A A A A A T A   T T T T G A A A A C   A A G T A A G T T T
99-1 1-9000  T T T A A A A A - -   - - C C G A A T A T   T A T C T A G G C T

                    6160              6170              6180
00-1 1-9000  C T A T G A T A C T   T C A T A A T A A T   A A G T A A T A A T
99-1 1-9000  G C A C G A C A C T   T T G C A A T A A T   A T G C A A T A G T

                    6190              6200              6210
00-1 1-9000  T A A T T G C T T A   A T C A T C A T C A   C A A C T A T T A T T
99-1 1-9000  C A A T A G T T A A   A C C A C T G C T G   C A A A C T C A T C

                    6220              6230              6240
00-1 1-9000  C G A A A C C A T A   A C T A T T C A A T   T T A A A A A G T A
99-1 1-9000  C A T A A T - A T A   A T C A C T G A G T   - - - - A A T A C
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Figure 53 cont'd

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                           6250                6260              6270
00-1 1-9000 A A A A A C A A T A   A C A T G G G A C A   A G T A G T T A T G
99-1 1-9000 A A A A T C A A G A   A A A T G G G A C A   A G T G G C T A T G

                           6280                6290              6300
00-1 1-9000 G A G G T G A A A G   T G G A G A A C A T   T C G A A C A A T A
99-1 1-9000 G A A G T A A G A G   T G G A G A A C A T   T C G A G C G A T A

                           6310                6320              6330
00-1 1-9000 G A T A T G C T C A   A A G C A A G A G T   A A A A A A T C G T
99-1 1-9000 G A C A T G T T C A   A A G C A A A G A T   A A A A A A C C G T

                           6340                6350              6360
00-1 1-9000 G T G G C A C G C A   G C A A A T G C T T   T A A A A A T G C C
99-1 1-9000 A T A A G A A G C A   G C A G G T G C T A   T A G A A A T G C T

                           6370                6380              6390
00-1 1-9000 T C T T T G G T C C   T C A T A G G A A T   A A C T A C A T T G
99-1 1-9000 A C A C T G A T C C   T T A T T G G A C T   A A C A G C G T T A

                           6400                6410              6420
00-1 1-9000 A G T A T T G C C C   T C A A T A T C T A   T C T G A T C A T A
99-1 1-9000 A G C A T G G C A C   T T A A T A T T T T   C C T G A T C A T C

                           6430                6440              6450
00-1 1-9000 A A C T A T A A A A   T G C A A A A A A A   C A C A T C T G A A
99-1 1-9000 G A T C A T G C A A   C A T T A A G A A A   C A T G A T C A A A

                           6460                6470              6480
00-1 1-9000 T C A G A A C A T C   A C A C C A G C T C   A T C A C C C A T G
99-1 1-9000 A C A G A A A A C T   G T G C T A A C A T   G C C G T C G G C A

                           6490                6500              6510
00-1 1-9000 G A A T C C A G C A   G A G A A C T C C   A A C G G T C C C C
99-1 1-9000 G A A C C A A G C A   A A A A G A C C C C   A A T G A C C T C C

                           6520                6530              6540
00-1 1-9000 A C A G A C A A C T   C A G A C A C C A A   C T C A A G C C C A
99-1 1-9000 A C A G C A G G C C   C A A A C A C C A A   A C C C A A T C C A

                           6550                6560              6570
00-1 1-9000 C A G C A T C C A A   C T C A A C A G T C   C A C A G A A G G C
99-1 1-9000 C A G C A A G C A A   C A C A G T G G A C   C A C A G A G A A C

                           6580                6590              6600
00-1 1-9000 T C C A C A C T C T   A C T T T G C A G C   C T C A G C A A G C
99-1 1-9000 T C A A C A T C C C   C A G T A G C A A C   C C C A G A G G G C

                           6610                6620              6630
00-1 1-9000 T C A C C A G A G A   C A G A A C C A A C   A T C A A C A C C A
99-1 1-9000 C A T C C A T A C A   C A G G G A C A A C   T C A A A C A T C A
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Figure 53 cont'd

Figure 53 cont'd

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                    .    .   . 7030          .    .   .  "7040"        .    .   .  7050
00-1 1-9000  A A G A T A A A A C C   A T G C A G A C A C   C A A C A A T G G A
99-1 1-9000  G A - - - A A A C C     A - - - - - A - - -   - - - - - - A - -

                    .    .   . 7060          .    .   .  7070           .    .   .  7080
00-1 1-9000  G A A G C C A A A A     G A C A A T T C A C   A A T C T C C C C A
99-1 1-9000  - A A A C C A A A A     C A T A A A C C C A   G A - - - C C C A  .

                    .    .   . 7090          .    .   .  7100           .    .   .  7110
00-1 1-9000  A A A A G G C A A C     A A C A C C A T A T   T A - - - G C T C T
99-1 1-9000  G A A A A C A T A       G A C A C C A T A T   G G A A G G T T C T

                    .    .   . 7120          .    .   .  7130           .    .   .  7140
00-1 1-9000  G C C C A A A T C T     C C C T G G A A A A   A A C A C T C G C C
99-1 1-9000  A G C A T A T G C A     C C A A T G A G A T   G G C A C T C G T T

                    .    .   . 7150          .    .   .  7160           .    .   .  7170
00-1 1-9000  C A T A T A C C A A     A A A T A C C A C A   A C C A C C C C A A
99-1 1-9000  C A T G T A T C A A     T A G C A C C A C C   A T C A T T C A A G

                    .    .   . 7180          .    .   .  7190           .    .   .  7200
00-1 1-9000  G A A A A A A A C T     G G G C A A A A C A   A C A C C C A A G A
99-1 1-9000  G A A T A A G A A G     A G G C A G A A - - - - A T T T A A G G

                    .    .   . 7210          .    .   .  7220           .    .   .  7230
00-1 1-9000  G A C A A A T A A C     A A T G G A T C C T   C T C A A T G A A T
99-1 1-9000  G A T A A A T G A C     A A T G A A C T C C C   T T T T G T G A A T

                    .    .   . 7240          .    .   .  7250           .    .   .  7260
00-1 1-9000  C C A C T G T T A T     T G T C T A T C T T   C C T G A C T C A T
99-1 1-9000  C T A C T G T T A A     T G T T T A T C T C   C C T G A T T C A T

                    .    .   . 7270          .    .   .  7280           .    .   .  7290
00-1 1-9000  A T C T T A A A G G     A G T G A T T T C C   T T T A G T G A G A
99-1 1-9000  A T C T C A A A G G     A G T A A T A T C T   T T T A G T G A A A

                    .    .   . 7300          .    .   .  7310           .    .   .  7320
00-1 1-9000  C T A A T G C A A T     T G G T T C A T G T   C T C T T A A A A A
99-1 1-9000  C C A A T G C A A T     T G G A T C A T G T   C T T T T G A A A A

                    .    .   . 7330          .    .   .  7340           .    .   .  7350
00-1 1-9000  G A C C T T A C C T     A A A A A A T G A C   A A C A C T G C A A
99-1 1-9000  G A C C C T A T C T     A A A A A A T G A C   A A C A C T G C C A

                    .    .   . 7360          .    .   .  7370           .    .   .  7380
00-1 1-9000  A A G T T G C C A T     A G A G A A T C C T   G T T A T C G A G C
99-1 1-9000  A A G T T G C T G T     A G A A A A C C C T   G T T G T T G A A C

                    .    .   . 7390          .    .   .  7400           .    .   .  7410
00-1 1-9000  A T G T T A G A C T     C A A A A A T G C A   G T C A A T T C T A
99-1 1-9000  A T G T G A G G C T     T A G A A A T G C A   G T C A T G A C C A
```

Figure 53 cont'd

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                              7420              7430              7440
00-1 1-9000   A G A T G A A A A T    A T C A G A T T A C    A A G A T A G T A G
99-1 1-9000   A A T G A A G A T      A T C A G A T T A T    A A A G T G G T T G

                              7450              7460              7470
00-1 1-9000   A G C C A G T A A A    C A T G C A A C A T    G A A A T T A T G A
99-1 1-9000   A A C C A G T T A A    T A T G C A G C A T    G A A A T A A T G A

                              7480              7490              7500
00-1 1-9000   A G A A T G T A C A    C A G T T G T G A G    C T C A C A T T A T
99-1 1-9000   A A A A T A T A C A    T A G T T G T G A G    C T T A C A T T A T

                              7510              7520              7530
00-1 1-9000   T A A A C A G T T      T T T A A C A A G G    A G T A A A A A T A
99-1 1-9000   T A A A C A A T T      C T T A A C G A G A    A G C A A A A A C A

                              7540              7550              7560
00-1 1-9000   T T A G C A C T C T    C A A A T T A A A T    A T G A T A T G T G
99-1 1-9000   T T A G C T C T C T    A A A A T T A A A T    A T G A T A T G T G

                              7570              7580              7590
00-1 1-9000   A T T G G C T G C A    G T T A A A G T C T    A C A T C A G A T G
99-1 1-9000   A T T G G T T A C A    G T T A A A A T C C    A C T T C A G A T A

                              7600              7610              7620
00-1 1-9000   A T A C C T C A A T    C C T A A G T T T T    A T A G A T G T A G
99-1 1-9000   A C A C A T C A A T    T C T C A A T T T T    A T A G A T G T G G

                              7630              7640              7650
00-1 1-9000   A A T T T A T A C C    T A G C T G G G T A    A G C A A T T G G T
99-1 1-9000   A G T T C A T A C C    C G T T T G G G T A    A G C A A T T G G T

                              7660              7670              7680
00-1 1-9000   T T A G T A A T T G    G T A C A A T C T C    A A C A A G T T G A
99-1 1-9000   T C A G T A A C T G    G T A T A A T C T C    A A T A A A T T A A

                              7690              7700              7710
00-1 1-9000   T T C T G G A A T T    C A G G A A A G A A    G A A G T A A T A A
99-1 1-9000   T C T T A G A G T T    T A G A A G A G A A    G A A G T A A T A A

                              7720              7730              7740
00-1 1-9000   G A A C T G G T T C    A A T C T T G T G T    A G G T C A T T G G
99-1 1-9000   G A A C T G G T T C    A A T T T T A T G T    A G A T C A C T A G

                              7750              7760              7770
00-1 1-9000   G T A A G T T A G T    T T T T G T T G T A    T C A T C A T A T G
99-1 1-9000   G C A A G T T A G T    T T T T A T T G T A    T C A T C T T A T G

                              7780              7790              7800
00-1 1-9000   G A T G T A T A G T    C A A G A G C A A C    A A A A G C A A A A
99-1 1-9000   G A T G T G T A G T    A A A A A G C A A C    A A A A G T A A A A
```

Figure 53 cont'd

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                        7810                    7820                    7830
00-1 1-9000    G A G T G A G C T T   C T T C A C A T A C   A A T C A A C T G T
99-1 1-9000    G A G T G A G C T T   T T T C A C C T A T   A A C C A A C T G T

                        7840                    7850                    7860
00-1 1-9000    T A A C A T G G A A   A G A T G T G A T G   T T A A G T A G A T
99-1 1-9000    T A A C A T G G A A   A G A T G T G A T G   T T A A G T A G A T

                        7870                    7880                    7890
00-1 1-9000    T C A A T G C A A A   T T T T T G T A T A   T G G G T A A G C A
99-1 1-9000    T C A A T G C A A A   C T T T T G T A T A   T G G G T A A G T A

                        7900                    7910                    7920
00-1 1-9000    A C A G T C T G A A   T G A A A A T C A A   G A A G G G C T A G
99-1 1-9000    A C A A C C T G A A   C A A A A A T C A A   G A A G G A C T A G

                        7930                    7940                    7950
00-1 1-9000    G G T T G A G A A G   T A A T C T G C A A   G G C A T A T T A A
99-1 1-9000    G A C T T A G A A G   C A A T C T G C A A   G G T A T G T T A A

                        7960                    7970                    7980
00-1 1-9000    C T A A T A A G C T   A T A T G A A A C T   G T A G A T T A T A
99-1 1-9000    C C A A T A A A T T   A T A T G A A A C T-   G T T G A T T A C A

                        7990                    8000                    8010
00-1 1-9000    T G C T T A G T T T   A T G T T G C A A T   G A A G G T T T C T
99-1 1-9000    T G C T A A G C C T   A T G C T G C A A T   G A A G G A T T C T

                        8020                    8030                    8040
00-1 1-9000    C A C T T G T G A A   A G A G T T C G A A   G G C T T T A T T A
99-1 1-9000    C T C T G G T G A A   A G A G T T T G A A   G G A T T T A T T A

                        8050                    8060                    8070
00-1 1-9000    T G A G T G A A A T   T C T T A G G A T T   A C T G A A C A T G
99-1 1-9000    T G A G T G A A A T   T C T A A A A A T T   A C T G A G C A T G

                        8080                    8090                    8100
00-1 1-9000    C T C A A T T C A G   T A C T A G A T T T   A G A A A T A C T T
99-1 1-9000    C T C A G T T C A G   T A C T A G G T T T   A G G A A T A C T T

                        8110                    8120                    8130
00-1 1-9000    T A T T A A A T G G   A T T A A C T G A A   C A A T T A A C A A
99-1 1-9000    T A T T G A A T G G   G T T A A C T G A A   C A A T T A T C A G

                        8140                    8150                    8160
00-1 1-9000    A A T T A A A A A A   T A A A A A C A G A   C T C A G A G T T C
99-1 1-9000    T G T T G A A A G C   T A A G A A C A G A   T C T A G A G T T C

                        8170                    8180                    8190
00-1 1-9000    A T G G T A C C G T   G T T A G A A A A T   A A T G A T T A T C
99-1 1-9000    T T G G A C T A T   A T T A G A A A A C   A A C A A T T A C C
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Figure 53 cont'd

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                        . 8200    .111/132.    8210          8220
00-1 1-9000  C A A T G T A C G A   A G T T G T A C T T   A A G T T A T T A G
99-1 1-9000  C T A T G T A C G A   A G T A G T A C T T   A A A T T A T T A G

                        . 8230              8240          . 8250
00-1 1-9000  G A G A T A C T T T   G A G A T G T A T T   A A A T T A T T A A
99-1 1-9000  G G G A C A C C T T   G A A A A G C A T A   A A G T T A T T A A .

                        . 8260              8270          . 8280
00-1 1-9000  T C A A T A A A A A   C T T A G A G A A T   G C T G C T G A A T
99-1 1-9000  T T A A C A A G A A   T T T A G A A A A T   G C T G C A G A A T

                        . 8290              8300          . 8310
00-1 1-9000  T A T A C T A T A T   A T T T A G A A T T   T T C G G T C A C C
99-1 1-9000  T A T A T T A T A T   A T T C A G A A T T   T T T G G A C A C C

                        . 8320              8330          . 8340
00-1 1-9000  C A A T G G T A G A   T G A A G A G A T   G C A A T G G A T G
99-1 1-9000  C T A T G G T A G A   T G A G A G G G A A   G C A A T G G A T G

                        . 8350              8360          . 8370
00-1 1-9000  C T G A T C A C T T   A A A C A A T G A A   A T C A C A A A A A
99-1 1-9000  C T G T C A A A T T   A A A C A A T G A G   A T T A C A A A A A

                        . 8380              8390          . 8400
00-1 1-9000  T C C T T A G G T G   G G A G A G C T T G   A C A G A A C T A A
99-1 1-9000  T T C T T A A A T T   A G A G A G T T T A   A C A G A A C T A A

                        . 8410              8420          . 8430
00-1 1-9000  G A G G G G C A T T   C A T A T T A A G G   A T T A T C A A A G
99-1 1-9000  G A G G A G C A T T   T A T A C T A A G A   A T T A T A A A A G

                        . 8440              8450          . 8460
00-1 1-9000  G A T T T G T A G A   C A A C A A C A A A   A G A T G G C C C A
99-1 1-9000  G G T T T G T A G A   C A A T A A T A A A   A G A T G G C C T A

                        . 8470              8480          . 8490
00-1 1-9000  A A A T T A A G A A   C T T A A A A G T G   C T T A G T A A G A
99-1 1-9000  A A A T T A A G A A   T T T A A A A G T G   C T C A G C A A A A

                        . 8500              8510          . 8520
00-1 1-9000  G A T G G A C T A T   G T A C T T C A A A   G C A A A A A G T T
99-1 1-9000  G A T G G G C A T A   G T A T T T C A A A   G C T A A A A G T T

                        . 8530              8540          . 8550
00-1 1-9000  A C C C C A G T C A   A C T T G A A T T A   A G C G A A C A A G
99-1 1-9000  A C C C T A G C C A   A C T T G A G C T A   A G T G T A C A A G

                        . 8560              8570          . 8580
00-1 1-9000  A T T T T T T A G A   G C T T G C T G C A   A T A C A G T T T G
99-1 1-9000  A T T T T T T A G A   A C T T G C T G C A   G T A C A A T T T G
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Figure 53 cont'd

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                      8590      .   .112/132.   .  .8600    .   .   .   .   .8610
00-1 1-9000  A A C A A G A G T T    T T C T G T C C T    G A A A A A A C C A
99-1 1-9000  A G C A G G A A T T    C T C T G T A C C T    G A A A A A A C C A

                      8620      .   .   .   .   .8630    .   .   .   .   .8640
00-1 1-9000  A C C T T G A G A T    G G T A T T A A A T    G A T A A A G C T A
99-1 1-9000  A C C T T G A G A T    G G T A T T A A A T    G A T A A A G C A A

                      8650      .   .   .   .   .8660    .   .   .   .   .8670
00-1 1-9000  T A T C A C C T C C    T A A A A G A T T A    A T A T G G T C T G
99-1 1-9000  T A T C A C C T C C    A A A A A G C T A    A T A T G G T C T G

                      8680      .   .   .   .   .8690    .   .   .   .   .8700
00-1 1-9000  T G T A T C A A A    A A A T T A C T T A    C C T G A G A A A A
99-1 1-9000  T A T A T C C A A A    A A A C T A C C T G    C C T G A A A C T A

                      8710      .   .   .   .   .8720    .   .   .   .   .8730
00-1 1-9000  T A A A A A A T C G    A T A T C T A G A A    G A G A C T T T C A
99-1 1-9000  T A A A A A A T C A    A T A T T T A G A A    G A G G C T T T C A

                      8740      .   .   .   .   .8750    .   .   .   .   .8760
00-1 1-9000  A T G C A A G T G A    T A G T C T C A A A    A C A A G A A G A G
99-1 1-9000  A T G C A A G T G A    C A G C C A A A G A    A C A A G G A G A G

                      8770      .   .   .   .   .8780    .   .   .   .   .8790
00-1 1-9000  T A C T A G A G T A    C T A T T T G A A A    G A T A A T A A A T
99-1 1-9000  T C T T A G A A T T    T T A C T A A A A    G A T T G T A A A T

                      8800      .   .   .   .   .8810    .   .   .   .   .8820
00-1 1-9000  T C G A C C A A A A    A G A A C T T A A A    A G T T A T G T T G
99-1 1-9000  T T G A T C A A A A    A G A A C T T A A A    C G T T A T G T A A

                      8830      .   .   .   .   .8840    .   .   .   .   .8850
00-1 1-9000  T T A A A C A A G A    A T A T T T A A A T    G A T A A G G A T C
99-1 1-9000  T T A A A C A A G A    G T A T C T G A A T    G A C A A A G A C C

                      8860      .   .   .   .   .8870    .   .   .   .   .8880
00-1 1-9000  A T A T T G T C T C    G C T A A C T G G A    A A A G A A A G A G
99-1 1-9000  A C A T T G T C T C    G T T A A C T G G G    A A G G A A G A G

                      8890      .   .   .   .   .8900    .   .   .   .   .8910
00-1 1-9000  A A T T A A G T G T    A G G T A G A A T G    T T T G C T A T G C
99-1 1-9000  A A T T A A G T G T    A G G T A G G A T G    T T T G C A A T G C

                      8920      .   .   .   .   .8930    .   .   .   .   .8940
00-1 1-9000  A A C C A G G A A A    A C A G C G A C A A    A T A C A A A T A T
99-1 1-9000  A A C C A G G A A A    A C A A A G C A G    A T A C A G A T A T

                      8950      .   .   .   .   .8960    .   .   .   .   .8970
00-1 1-9000  T G G C T G A A A A    A T T G T T A G C T    G A T A A T A T T G
99-1 1-9000  T A G C T G A G A A    A C T T C T A G C T    G A T A A T A T T G
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Figure 53 cont'd

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                      . . . . . 8980 . . . 113/132. . . . . 8990 . . . . . . . . . 9000
00-1 1-9000  T A C C T T T T T T    C C C A G A A A C C    T T A A C A A A G T
99-1 1-9000  T A C C T T T T T T    C C C A G A A A C T    T T A A C A A A G T

             . . . . . . . . . 9010 . . . . . . . . . 9020 . . . . . . . . . 9030
00-1 1-9000  A T G G T G A T C T    A G A T C T T C A G    A G A A T A A T G G
99-1 1-9000  A T G G T G A C T T    A G A T C T C C A A    A G A A T T A T G G

             . . . . . . . . . 9040 . . . . . . . . . 9050 . . . . . . . . . 9060
00-1 1-9000  A A A T C A A A T C    G G A A C
99-1 1-9000  A A A T A A A A T C    A G A A C T T T C T    T C C A T T A A A A

             . . . . . . . . . 9070 . . . . . . . . . 9080 . . . . . . . . . 9090
00-1 1-9000
99-1 1-9000  C T A G A A A G A A    T G A T A G C T A C    A A C A A T T
```

Figure 53 cont'd

WO 03/072719   114/132   PCT/US03/05271

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                   1            10                      20                          30
00-1 7001-13350  A C A A T G G A G A   A G C C A A A A G A   C A A T T C A C A A
99-1 7001-13294  - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -

                              40                      50                          60
00-1 7001-13350  T C T C C C A A A   A A G G C A A C A A   C A C C A T A T T A
99-1 7001-13294  - - - - - - - - -   - A A A C A T A G A   C A C C A T A T G G

                              70                      80                          90
00-1 7001-13350  G C T C T G C   C C A A A T C T C C   C T G G A A A A A A
99-1 7001-13294  A A G G T T C T A G   C A T A T G C A C C   A A T G A G A T G G

                             100                     110                         120
00-1 7001-13350  C A C T C G C C C A   T A T A C C A A A A   A T A C C A C A A C
99-1 7001-13294  C A T C T G T T C A   T A T C A T C A A T A   G C A C C A C C A T

                             130                     140                         150
00-1 7001-13350  C A C C C C A A G A   A A A A A A C T G G   G C A A A A C A A C
99-1 7001-13294  C A T T C A A G G A   A T A A G A A G A G   G C G A A A - - - -

                             160                     170                         180
00-1 7001-13350  A C C C A A G A G A   C A A A T A A C A A   T G G A T C C T C T
99-1 7001-13294  A T T T A A G G A   T A A A T G A C A A   T G G A T C C C T T

                             190                     200                         210
00-1 7001-13350  C A A T G A A T C C   A C T G T T A A T G   T C T A T C T T C C
99-1 7001-13294  T T G T G A A T C T   A C T G T T A A T G   T T T A T C T C C C

                             220                     230                         240
00-1 7001-13350  T G A C T C A T A T   C T T A A A G G A G   T G A T T T C C T T
99-1 7001-13294  T G A T T C A T A T   C T C A A A G G A G   T A A T A T C T T T

                             250                     260                         270
00-1 7001-13350  T A G T G A G A C T   A A T G C A A T T G   G T T C A T G T C T
99-1 7001-13294  T A G T G A A A C C   A A T G C A A T T G   G A T C A T G T C T

                             280                     290                         300
00-1 7001-13350  C T T A A A A A G A   C C T T A C T A A   A A A A T G A C A A
99-1 7001-13294  T T T G A A A A G A   C C C T A T C T A A   A A A A T G A C A A

                             310                     320                         330
00-1 7001-13350  C A C T G C A A A A   G T T G C A T A G   A G A A T C C T G T
99-1 7001-13294  C A C T G C C A A A   G T T G C T G T A G   A A A A C C C T G T

                             340                     350                         360
00-1 7001-13350  T A T C G A G C A T   G T T A G A C T C A   A A A A T G C A G T
99-1 7001-13294  T G T T G A A C A T   G T G A G G C T T A   G A A A T G C A G T

                             370                     380                         390
00-1 7001-13350  C A A T T C T A A G   A T G A A A A T A T   C A G A T T A C A A
99-1 7001-13294  C A T G A C C A A A   A T G A A G A T A T   C A G A T T A T A A
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Figure 53 cont'd

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                                400                    410                    420
00-1 7001-13350  G A T A G T A G A G   C C A G T A A A C A   T G C A A C A T G A
99-1 7001-13294  A G T G G T T G A A   C C A G T T A A T A   T G C A G C A T G A

                                430                    440                    450
00-1 7001-13350  A A T T A T G A A G   A A T G T A C A C A   G T T G T G A G C T
99-1 7001-13294  A A T A A T G A A A   A A T A T A C A T A   G T T G T G A G C T

                                460                    470                    480
00-1 7001-13350  C A C A T T A T T A   A A A C A G T T T T   T A A C A A G G A G
99-1 7001-13294  T A C A T T A T T A   A A A C A A T T C T   T A A C G A G A G

                                490                    500                    510
00-1 7001-13350  T A A A A T A T T   A G C A C T C T C A   A A T T A A A T A T
99-1 7001-13294  C A A A A C A T T   A G C T C T C T A A   A A T T A A A T A T

                                520                    530                    540
00-1 7001-13350  G A T A T G T G A T   T G G C T G C A G T   T A A A G T C T A C
99-1 7001-13294  G A T A T G T G A T   T G G T T A C A G T   T A A A A T C C A C

                                550                    560                    570
00-1 7001-13350  A T C A G A T G A T   A C C T C A A T C C   T A A G T T T T A T
99-1 7001-13294  T T C A G A T A A C   A C A T C A A T T C   T C A A T T T A T

                                580                    590                    600
00-1 7001-13350  A G A T G T A G A A   T T T A T A C C T A   G C T G G G T A A G
99-1 7001-13294  A G A T G T G G A G   T T C A T A C C C G   T T T G G G T A A G

                                610                    620                    630
00-1 7001-13350  C A A T T G G T T T   A G T A A T T G G T   A C A A T C T C A A
99-1 7001-13294  C A A T T G G T T C   A G T A A C T G G T   A T A A T C T C A A

                                640                    650                    660
00-1 7001-13350  C A A G T T G A T T   C T G G A A T T C A   G G A A A G A A G A
99-1 7001-13294  T A A A T T A A T C   T T A G A G T T T A   G A A G A G A A G A

                                670                    680                    690
00-1 7001-13350  A G T A A T A A G A   A C T G G T T C A A   T C T T G T G T A G
99-1 7001-13294  A G T A A T A A G A   A C T G G T T C A A   T T T T A T G T A G

                                700                    710                    720
00-1 7001-13350  G T C A T T G G G T   A A A T T A G T T T   T T G T T G T A T C
99-1 7001-13294  A T C A C T A G G C   A A G T T A G T T T   T T A T T G T A T C

                                730                    740                    750
00-1 7001-13350  A T C A T A T G G A   T G T A T A G T C A   A G A G C A A C A A
99-1 7001-13294  A T C T T A T G G A   T G T G T A G T A A   A A A G C A A C A A

                                760                    770                    780
00-1 7001-13350  A A G C A A A A G A   G T G A G C T T C T   T C A C A T A C A A
99-1 7001-13294  A A G T A A A A G A   G T G A G C T T T T   T C A C C T A T A A
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Figure 53 cont'd

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                                    790                        890                        810
00-1 7001-13350   T C A A C T G T T A     A C A T G G A A A G     A T G T G A T G T T
99-1 7001-13294   C C A A C T G T T A     A C A T G G A A A G     A T G T G A T G T T

                                    820                        830                        840
00-1 7001-13350   A A G T A G A T T C     A A T G C A A A T T     T T T G T A T A T G
99-1 7001-13294   A A G T A G A T T C     A A T G C A A A C T     T T T G T A T A T G

                                    850                        860                        870
00-1 7001-13350   G G T A A G C A A C     A G T C T G A A T G     A A A A T C A A G A
99-1 7001-13294   G G T A A G T A A C     A A C C T G A A C A     A A A A T C A A G A

                                    880                        890                        900
00-1 7001-13350   A G G G C T A G G G     T T G A G A A G T A     A T C T G C A A G G
99-1 7001-13294   A G G A C T A G G A     C T T A G A A G C A     A T C T G C A A G G

                                    910                        920                        930
00-1 7001-13350   C A T A T T A A C T     A A T A A G C T A T     A T G A A A C T G T
99-1 7001-13294   T A T G T T A A C C     A A T A A A T T A T     A T G A A A C T G T

                                    940                        950                        960
00-1 7001-13350   A G A T T A T A T G     C T T A G T T T A T     G T T G C A A T G A
99-1 7001-13294   T G A T T A C A T G     C T A A G C C T A T     G C T G C A A T G A

                                    970                        980                        990
00-1 7001-13350   A G G T T T C T C A     C T T G T G A A A G     A G T T C G A A G G
99-1 7001-13294   A G G A T T C T C T     C T G G T G A A A G     A G T T T G A A G G

                                    1000                       1010                       1020
00-1 7001-13350   C T T T A T T A T G     A G T G A A A T T C     T T A G G A T T A C
99-1 7001-13294   A T T T A T T A T G     A G T G A A A T T C     T A A A A A T T A C

                                    1030                       1040                       1050
00-1 7001-13350   T G A A C A T G C T     C A A T T C A G T A     C T A G A T T T A G
99-1 7001-13294   T G A G C A T G C T     C A G T T C A G T A     C T A G G T T A G

                                    1060                       1070                       1080
00-1 7001-13350   A A A T A C T T T A     T T A A A T G G A T     T A A C T G A T C A
99-1 7001-13294   G A A T A C T T T A     T T G A A T G G G T     T A A C T G A A C A

                                    1090                       1100                       1110
00-1 7001-13350   A T T A A C A A A A     T T A A A A A T A     A A A A C A G A C T
99-1 7001-13294   A T T A T C A G T G     T T G A A A G C T A     A G A A C A G A T C

                                    1120                       1130                       1140
00-1 7001-13350   C A G A G T T C A T     G G T A C C G T G T     T A G A A A A T A A
99-1 7001-13294   T A G A G T T C T T     G G A A C T A T A T     T A G A A A A C A A

                                    1150                       1160                       1170
00-1 7001-13350   T G A T T A T C C A     A T G T A C G A A G     T T G T A C T T A A
99-1 7001-13294   C A A T T A C C C T     A T G T A C G A A G     T A G T A C T T A A
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Figure 53 cont'd

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                                    1180              1190                1200
00-1 7001-13350  G T T A T T A G G A  G A T A C T T T G A  G A T G T A T T A A
99-1 7001-13294  A T T A T T A G G G  G A C A C C T T G A  A A A G C A T A A A

                                    1210              1220                1230
00-1 7001-13350  A T T A T T A A T C  A A T A A A A C T  T A G A G A A T G C
99-1 7001-13294  G T T A T T A A T T  A A C A A G A A T T  T A G A A A A T G C

                                    1240              1250                1260
00-1 7001-13350  T G C T G A A T T A  T A C T A T A T A T  T T A G A A T A T T
99-1 7001-13294  T G C A G A A T T A  T A T T A T A T A T  T C A G A A T T T T

                                    1270              1280                1290
00-1 7001-13350  C G G T C A C C C A  A T G G T A G A T G  A A A G A G A T G C
99-1 7001-13294  T G G A C A C C C T  A T G G T A G A T G  A G A G G G A A G C

                                    1300              1310                1320
00-1 7001-13350  A A T G G A T G C T  G T C A A T T A A  A C A A T G A A A T
99-1 7001-13294  A A T G G A T G C T  G T T A A T T A A  A C A A T G A G A T

                                    1330              1340                1350
00-1 7001-13350  C A C A A A A A T C  C T T A G G T G G G  A G A G C T T G A C
99-1 7001-13294  T A C A A A A A T T  C T T A A A T T A G  A G A G T T A A C

                                    1360              1370                1380
00-1 7001-13350  A G A A C T A A G A  G G G G C A T T C A  T A T T A A G G A T
99-1 7001-13294  A G A A C T A A G A  G G A G C A T T T A  T A C T A A G A A T

                                    1390              1400                1410
00-1 7001-13350  T A T C A A G G A  T T T G T A G A C A  A C A A C A A A G
99-1 7001-13294  T A T A A A G G G  T T T G T A G A C A  A T A A T A A A G

                                    1420              1430                1440
00-1 7001-13350  A T G G C C C A A A  A T T A A A A C T  T A A A A G T G C T
99-1 7001-13294  A T G G C C T A A A  A T T A A G A A T T  T A A A A G T G C T

                                    1450              1460                1470
00-1 7001-13350  T A G T A A G A G A  T G G A C T A T G T  A C T T C A A A G C
99-1 7001-13294  C A G C A A A A G A  T G G G C T A T G T  A T T T C A A A G C

                                    1480              1490                1500
00-1 7001-13350  A A A A A G T T A C  C C C A G T C A A C  T T G A A T T A A G
99-1 7001-13294  T A A A A G T T A C  C C T A G C C A A C  T T G A G C T A A G

                                    1510              1520                1530
00-1 7001-13350  C G A A C A A G A T  T T T T A G A G C  T T G C T G C A A T
99-1 7001-13294  I G T A C A A G A T  T T T T A G A A C  T T G C T G C A G T

                                    1540              1550                1560
00-1 7001-13350  A C A G T T T G A A  C A A G A G T T T T  C T G T C C C T G A
99-1 7001-13294  A C A A T T T G A G  C A G G A A T T C T  C T G T A C C T G A
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Figure 53 cont'd

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                                    1570                    1580                    1590
00-1 7001-13350   A A A A A C C A A C   C T T G A G A T G G   T A T T A A A T G A
99-1 7001-13294   A A A A A C C A A C   C T T G A G A T G G   T A T T A A A T G A

                                    1600                    1610                    1620
00-1 7001-13350   T A A A G C T A T A   T C A C C T C C T A   A A A G A T T A A T
99-1 7001-13294   T A A A G C A A T A   T C A C C T C C A A   A A A G C T A A T

                                    1630                    1640                    1650
00-1 7001-13350   A T G G T C T G T G   T A T C C A A A A A   A T T A C T T A C C
99-1 7001-13294   A T G G T C T G T A   T A T C C A A A A A   A C T A C C T G C C

                                    1660                    1670                    1680
00-1 7001-13350   T G A G A A A A T A   A A A A A T C G A T   A T C T A G A A G A
99-1 7001-13294   T G A A A C T A T A   A A A A A T C A A T   A T T T A G A A G A

                                    1690                    1700                    1710
00-1 7001-13350   G A C T T T C A A T   G C A A G T G A T A   G T C T C A A A A C
99-1 7001-13294   G G C T T T C A A T   G C A A G T G A C A   G C C A A A G A A C

                                    1720                    1730                    1740
00-1 7001-13350   A A G A A G A G T A   C T A G A G T A C T   A T T T G A A A G A
99-1 7001-13294   A A G G A G A G T C   T T A G A A T T T T   A C T A A A A G A

                                    1750                    1760                    1770
00-1 7001-13350   T A A T A A A T T C   G A C C A A A A A G   A A C T T A A A A G
99-1 7001-13294   T T G T A A A T T T   G A T C A A A A A G   A A C T T A A A C G

                                    1780                    1790                    1800
00-1 7001-13350   T T A T G T T G T T   A A A C A G A A T   A T T T A A A T G A
99-1 7001-13294   T T A T G T A A T T   A A A C A G A G T   A T C T G A A T G A

                                    1810                    1820                    1830
00-1 7001-13350   T A A G G A T C A T   A T T G T C T C G C   T A A C T G G A A A
99-1 7001-13294   C A A A G A C C A C   A T T G T C T C G T   T A A C T G G G A A

                                    1840                    1850                    1860
00-1 7001-13350   A G A A A G A G A A   T T A A G T G T A G   G T A G A A T G T T
99-1 7001-13294   G G A A A G A G A A   T T A A G T G T A G   G T A G A A T G T T

                                    1870                    1880                    1890
00-1 7001-13350   T G C T A T G C A A   C C A G G A A A A C   A G C G A C A A A T
99-1 7001-13294   T G C A A T G C A A   C C A G G A A A A C   A A A G A C A G A T

                                    1900                    1910                    1920
00-1 7001-13350   A C A A A T A T T G   G C T G A G A A A C   T G T T A G C T G A
99-1 7001-13294   A C A G A T A T T A   G C T G A G A A A C   T T C T A G C T A

                                    1930                    1940                    1950
00-1 7001-13350   T A A T A T T G T A   C C T T T T T T C C   C A G A A A C C T T
99-1 7001-13294   T A A T A T T G T A   C C T T T T T T C C   C A G A A A C T T T
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Figure 53 cont'd

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                        1960                    1970                    1980
00-1 7001-13350  A A C A A A G T A T    G G T G A T C T A G    A T C T T C A G A G
99-1 7001-13294  A A C A A A G T A T    G G T G A C T T A G    A T C T C C A A A G

                        1990                    2000                    2010
00-1 7001-13350  A A T A A T G G A A    A T C A A A T C G G    A A C T T T C T T C
99-1 7001-13294  A A T T A T G G A A    A T A A A A T C A G    A A C T T T C T T C

                        2020                    2030                    2040
00-1 7001-13350  T A T T A A A A C T    A G A A G A A A T G    A T A G T T A T A A
99-1 7001-13294  C A T T A A A A C T    A G A A G A A T G     A T A G C T A C A A

                        2050                    2060                    2070
00-1 7001-13350  T A A T T A C A T T    G C A A G A G C A T    C C A T A G T A A C
99-1 7001-13294  C A A T T A T A T T    C A A G G G C C T     C T A T A G T A A G

                        2080                    2090                    2100
00-1 7001-13350  A G A T T T A A G T    A A G T T C A A C C    A A G C C T T T A G
99-1 7001-13294  A G A C T T A A G T    A A G T T C A A T C    A G G C C T T T A G

                        2110                    2120                    2130
00-1 7001-13350  G T A T G A A A C T    A C A G C G A T C T    G T G C G G A T G T
99-1 7001-13294  A T A T G A A A C C    A C A G C T A T A T    G T G C A G A T G T

                        2140                    2150                    2160
00-1 7001-13350  A G C A G A T G A A    C T A C A T G G A A    C A C A A A G C C T
99-1 7001-13294  A G C T G A T G A G    T T A C A T G G G A    C A C A A A G C T T

                        2170                    2180                    2190
00-1 7001-13350  A T T C T G T T G G    T T A C A T C T T A    T C G T C C C T A T
99-1 7001-13294  A T T C T G T T G G    T T A C A T C T T A    T T G T T C C C A T

                        2200                    2210                    2220
00-1 7001-13350  G A C A A C A A T G    A T A T G T G C C T    A T A G A C A T G C
99-1 7001-13294  G A C T A C A A T G    A T A T G T G C A T    A C A G A C A T G C

                        2230                    2240                    2250
00-1 7001-13350  A C C A C C A G A A    A C A A A A G G T G    A A T A T G A T A T
99-1 7001-13294  A C C A C C A G A A    A C A A A A G G G G    A A T A T A T A T

                        2260                    2270                    2280
00-1 7001-13350  A G A T A A G A T A    G A A G A G C A A A    G T G G T T T A T A
99-1 7001-13294  A G A C A A A A T A    C A A G A G C A A A    G C G G A T T A T A

                        2290                    2300                    2310
00-1 7001-13350  T A G A T A T C A T    A T G G G T G G T A    T T G A A G G A T G
99-1 7001-13294  C A G A T A T C A T    A T G G G A G G G A    T T G A A G G G T G

                        2320                    2330                    2340
00-1 7001-13350  G T G T C A A A A A    C T C T G G A C A A    T G G A A G C T A T
99-1 7001-13294  G T G C C A G A A G    T T A T G G A C A A    T G G A A G C A A T
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Figure 53 cont'd

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                              2350                    2360                    2370
00-1 7001-13350  A T C T C T A T T A    G A T G T T G T A T    C T G T A A A A A C
99-1 7001-13294  A T C C T T G T T A    G A T G T A G T A T    C T G T G A A G A C

                              2380                    2390                    2400
00-1 7001-13350  A C G A T G T C A A    A T G A C A T C T T    T A T T A A A C G G
99-1 7001-13294  T C G C T G T C A G    A T G A C C T C T C    T A T T A A A C G G

                              2410                    2420                    2430
00-1 7001-13350  T G A C A A C C A A    T C A A T A G A T G    T A A G T A A A C C
99-1 7001-13294  A G A C A A T C A G    T C A A T A G A T G    T T A G T A A A C C

                              2440                    2450                    2460
00-1 7001-13350  A G T T A A G T T A    T C T G A G G G T T    T A G A T G A A G T
99-1 7001-13294  A G T A A A A T T G    T C T G A A G G T A    T A G A T G A A G T

                              2470                    2480                    2490
00-1 7001-13350  G A A A G C A G A T    T A T A G C T T G G    C T G T A A A A A T
99-1 7001-13294  A A A A G C A G A C    T A T A G C T T A G    C A A T T A G A A T

                              2500                    2510                    2520
00-1 7001-13350  G T T A A A G A A    A T A A G A G A T G    C A T A C A G A A A
99-1 7001-13294  G C T T A A A G A A    A T A A G A G A T G    C T T A T A A A A A

                              2530                    2540                    2550
00-1 7001-13350  T A T A G G C C A T    A A A C T T A A A G    A A G G G G A A A C
99-1 7001-13294  C A T T G G T C A T    A A A C T C A A A G    A A G G T G A A A C

                              2560                    2570                    2580
00-1 7001-13350  A T A T A T A T C A    A G A G A T C T T C    A G T T T A T A A G
99-1 7001-13294  A T A T A T A T C A    A G G G A T C T C C    A A T T T A T A A G

                              2590                    2600                    2610
00-1 7001-13350  T A A G G T G A T T    C A A T C T G A A G    G A G T C A T G C A
99-1 7001-13294  T A A G G T G A T T    C A A T C T G A A G    G A G T C A T G C A

                              2620                    2630                    2640
00-1 7001-13350  T C C T A C C C C T    A T A A A A A A G A    T C T T A A G A G T
99-1 7001-13294  T C C T A C C C C T    A T A A A A A A G A    T A T T A A G A G T

                              2650                    2660                    2670
00-1 7001-13350  G G G A C C A T G G    A T A A A C A C A A    T A T T A G A T G A
99-1 7001-13294  A G G T C C T T G G    A T A A A T A C A A    T A C T A G A T G A

                              2680                    2690                    2700
00-1 7001-13350  C A T T A A A A C C    A G T G C A G A G T    C A A T A G G G A G
99-1 7001-13294  T A T T A A A A C C    A G T G C A G A A T    C A A T A G G A A G

                              2710                    2720                    2730
00-1 7001-13350  T C T A T G T C A G    G A A T T A G A A T    T T A G G G G G G A
99-1 7001-13294  T C T A T G T C A A    G A A C T A G A A T    T C A G A G G G G A
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Figure 53 cont'd

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                            2740                2750                2760
00-1 7001-13350   A A G C A T A A T A   G T T A G T C T G A   T A T T A A G G A A
99-1 7001-13294   G A G T A T A C T A   G T T A G C T T G A   T A T T A A G G A A

                            2770                2780                2790
00-1 7001-13350   T T T T T G G C T G   T A T A A T T T A T   A C A T G C A T G A
99-1 7001-13294   T T T C T G G C T G   T A T A A C T T G T   A C A T G T A T G A

                            2800                2810                2820
00-1 7001-13350   A T C A A A G C A A   C A C C C C C T A G   C A G G G A A G C A
99-1 7001-13294   G T C A A A A C A G   C A C C C A T T A G   C T G G G A A G C A

                            2830                2840                2850
00-1 7001-13350   G T T A T T C A A A   C A A C T A A A T A   A A A C A T T A A C
99-1 7001-13294   A C T T T C A A G   C A A T T G A A C A   A A A C A T T A A C

                            2860                2870                2880
00-1 7001-13350   A T C A G T G C A G   A G A T T T T T T G   A A A T A A A A A A
99-1 7001-13294   A T C T G T G C A G   A G A T T T T T G   A A C T G A A G A A

                            2890                2900                2910
00-1 7001-13350   G G A A A A T G A A   G T A G T A G A T C   T A T G G A T G A A
99-1 7001-13294   A G A A A A T G A T   G T G G T T G A C C   T A T G G A T G A A

                            2920                2930                2940
00-1 7001-13350   C A T A C C A A T G   C A G T T T G G A G   G A G G A G A T C C
99-1 7001-13294   T A T A C C A A T G   C A G T T T G G A G   G G G G A G A T C C

                            2950                2960                2970
00-1 7001-13350   A G T A G T C T T C   T A T A G A T C T T   T C T A T A G A A G
99-1 7001-13294   A G T A G T T T T T   T A C A G A T C T T   T T T A C A G A A G

                            2980                2990                3000
00-1 7001-13350   G A C C C C T G A T   T T T T T A A C T G   A A G C A A T C A G
99-1 7001-13294   G A C T C C G A T T   T T C C T A A C T G   A A G C A A T C A G

                            3010                3020                3030
00-1 7001-13350   T C A T G T G G A T   A T T C T G T T A A   G A A T A T C A G C
99-1 7001-13294   C C A T G T G G A T   T T A C T G T T A A   A A G T G T C A A A

                            3040                3050                3060
00-1 7001-13350   C A A C A T A A G A   A A T G A A G C G A   A A A T A G T T T
99-1 7001-13294   C A A T A T C A A A   G A T G A G A C T A   A G A T A C C A T T

                            3070                3080                3090
00-1 7001-13350   C T T C A A A G C C   T T A C T G T C T A   T A G A A A A A A A
99-1 7001-13294   T T T C A A A G C C   T T A T T A T C T A   T A G A A A G A A

                            3100                3110                3120
00-1 7001-13350   T G A A C G T G C T   A C A C T G A C A A   C A C T A A T G A G
99-1 7001-13294   T G A A C G T G C T   A C A T T A A C A A   C A C T A A T G A G
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Figure 53 cont'd

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                              3130              3140              3150
00-1 7001-13350  A G A T C C T C A A   G C T G T T G G C T   C A G A G C G A C A
99-1 7001-13294  A G A C C C T C A G   G C A G T A G G A T   C A G A A C G A C A

                              3160              3170              3180
00-1 7001-13350  A G C A A A A G T A   A C A A G T G A T A   T C A A T A G A A C
99-1 7001-13294  A G C T A A G G T A   A C A A G T G A T A   T A A A T A G A A C

                              3190              3200              3210
00-1 7001-13350  A G C A G T T A C C   A G C A T C T T A A   G T C T T T C T C C
99-1 7001-13294  A G C A G T T A C C   A G C A T A C T G A   G T C T A T C T C C

                              3220              3230              3240
00-1 7001-13350  A A A T C A A C T T   T T C A G C G A T A   G T G C T A T A C A
99-1 7001-13294  A A A T C A G C T C   T T C T G T G A T A   G T G C T A T A C A

                              3250              3260              3270
00-1 7001-13350  C T A C A G T A G A   A A T G A A G A A G   A G G T C G G A A T
99-1 7001-13294  T T A T A G T A G A   A A T G A G G A A G   A A G T T G G G A T

                              3280              3290              3300
00-1 7001-13350  C A T T G C T G A C   A A C A T A A C A C   C T G T T T A T C C
99-1 7001-13294  C A T T G C A G A C   A A C A T A A C A C   C T G T C T A T C C

                              3310              3320              3330
00-1 7001-13350  T C A T G G A C T G   A G A G T T T T G T   A T G A A T C A T T
99-1 7001-13294  T C A T G G G C T G   A G A G T G C T C T   A T G A A T C A C T

                              3340              3350              3360
00-1 7001-13350  A C C T T T T C A T   A A A G C T G A A A   A A G T T G T G A A
99-1 7001-13294  A C C T T T T C A T   A A G G C T G A A A   A G G T T G T C A A

                              3370              3380              3390
00-1 7001-13350  T A T G A T A T C A   G G A A C G A A A T   C C A T A A C C A A
99-1 7001-13294  T A T G A T A T C A   G G C A C A A A G T   C T A T A A C T A A

                              3400              3410              3420
00-1 7001-13350  C T T A T T A C A G   A G A A C A T C T G   C T A T T A A T G G
99-1 7001-13294  T C T T A T T A C A G   A G A A C A T C T G   C T A T C A T T G G

                              3430              3440              3450
00-1 7001-13350  T G A A G A T A T T   G A C A G A G C T G   I A T C C A T G A T
99-1 7001-13294  T G A A G A T A T T   G A T A G A G C A G   I G T C T A T G A T

                              3460              3470              3480
00-1 7001-13350  G C T G G A G A A C   C T A G A G A T T A T   T A T C T A G A A T
99-1 7001-13294  G T T A G A G A A C   T T A G G G T T G T   T A T C T A G A A T

                              3490              3500              3510
00-1 7001-13350  A T T G T C A G T A   G T T G T T G A T A   G T A T A G A A A T
99-1 7001-13294  A T T G T C A G T A   A T A A T T A A T A   G T A T A G A A A T
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Figure 53 cont'd

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                              3520                    3530                    3540
00-1 7001-13350  T C C A A C C A A A    T C T A A T G G T A    G G C T G A T A T G
99-1 7001-13294  A C C A A T C A A G    T C C A A T G G C A    G A T T G A T A T G

                              3550                    3560                    3570
00-1 7001-13350  T T G T C A G A T A    T C T A G A A C C C    T A A G G G A G A C
99-1 7001-13294  C T G T C A A A T T    T C C A A G A C C T    T G A G A G A A A A

                              3580                    3590                    3600
00-1 7001-13350  A T C A T G G A A T    A A T A T G G A A A    T A G T T G G A G T
99-1 7001-13294  A T C A T G G A A C    A A T A T G G A A A    T A G T A G G A G T

                              3610                    3620                    3630
00-1 7001-13350  A A C A T C C C C T    A G C A T C A C T A    C A T G C A T G G A
99-1 7001-13294  G A C A T C T C C T    A G T A T T G T G A    C A T G T A T G G A

                              3640                    3650                    3660
00-1 7001-13350  T G T C A T A T A T    G C A A C T A G C T    C T C A T T T G A A
99-1 7001-13294  T G T T G T G T A T    G C A A C T A G T T    C T C A T T T A A A

                              3670                    3680                    3690
00-1 7001-13350  A G G G A T A A T C    A T T G A A A A G T    T C A G C A C T G A
99-1 7001-13294  A G G A A T A A T T    A T T G A A A A A T    T C A G T A C T G A

                              3700                    3710                    3720
00-1 7001-13350  C A G A A C T A C A    A G A G G T C A A A    G A G G T C C A A A
99-1 7001-13294  C A A G A C C A C A    A G A G G T C A G A    G G G G A C C A A A

                              3730                    3740                    3750
00-1 7001-13350  G A G C C C T T G G    G T A G G G T C G A    G C A C T C A A G A
99-1 7001-13294  A A G C C C C T G G    G T A G G A T C A A    G C A C T C A A G A

                              3760                    3770                    3780
00-1 7001-13350  G A A A A A A T T A    G T T C C T G T T T    A T A A C A G A C A
99-1 7001-13294  G A A A A A A T T G    G T T C C T G T T T    A T A A T A G A C A

                              3790                    3800                    3810
00-1 7001-13350  A A T T C T T T C A    A A A C A A C A A A    G A G A A C A G C T
99-1 7001-13294  A A T T C T T T C A    A A A C A A C A A A    A A G A C A A C T

                              3820                    3830                    3840
00-1 7001-13350  A G A A G C A A T T    G G A A A A A T G A    G A T G G G T A T A
99-1 7001-13294  G G A A G C A A T A    G G G A A A T G A    G G T G G G T G T A

                              3850                    3860                    3870
00-1 7001-13350  T A A A G G A C A    C C A G G T T T A A    G A C G A T T A C T
99-1 7001-13294  C A A A G G A C T    C C A G G G C T A A    G A A G A T T G C T

                              3880                    3890                    3900
00-1 7001-13350  C A A T A A G A T T    T G T C T T G G A A    G T T T A G G C A T
99-1 7001-13294  C A A C A A G A T T    T G C A T A G G A A    G C T T A G G T A T
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Figure 53 cont'd

Figure 53 cont'd

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                                4300                    4310                    4320
00-1 7001-13350  C A A A A T A G A T    A T G T T A A C A C    T G G G G A A A A T
99-1 7001-13294  C A A A A T A G A C    A T A T T A A C A C    T A G G G A A G A T

                                4330                    4340                    4350
00-1 7001-13350  G C T C A T G C C C    A C T A T A A A A G    G T C A G A A A A C
99-1 7001-13294  G C T T A T G C C T    A C C A T A A A A G    G T C A A A A A C

                                4360                    4370                    4380
00-1 7001-13350  A G A T C A G T T C    C T G A A C A A G A    G A G A G A A T T A
99-1 7001-13294  T G A T C A G T T C    T T A A A C A A G A    G A G A A A C T A

                                4390                    4400                    4410
00-1 7001-13350  T T T C C A T G G G    A A T A A T C T T A    T T G A G T C T T T
99-1 7001-13294  T T T T C A T G G A    A A T A A T T T A A    T T G A A T C T T T

                                4420                    4430                    4440
00-1 7001-13350  G T C A G C A G C G    T T A G C A T G T C    A T T G G T G T G G
99-1 7001-13294  A T C T G C A G C A    C T T G C A T G C C    A C T G G T G T G G

                                4450                    4460                    4470
00-1 7001-13350  G A T A T T A A C A    G A G C A A T G T A    T A G A A A A A A
99-1 7001-13294  G A T A T T A A C A    G A A C A G T G C A    T A G A A A A C A A

                                4480                    4490                    4500
00-1 7001-13350  T A T T T T C A A G    A A A G A C T G G G    G T G A C G G G T T
99-1 7001-13294  T A T C T T T A G G    A A A G A T T G G G    G T G A T G G G T T

                                4510                    4520                    4530
00-1 7001-13350  C A T A T C G G A T    C A T G C T T T T A    T G G A C T T C A A
99-1 7001-13294  C A T C T C A G A T    C A T G C C T T C A    T G G A T T T C A A

                                4540                    4550                    4560
00-1 7001-13350  A A T A T T C C T A    T G T G T C T T T A    A A A C T A A A C T
99-1 7001-13294  G G T A T T T C T A    T G T G T A T T T A    A A A C C A A A C T

                                4570                    4580                    4590
00-1 7001-13350  T T T A T G T A G T    T G G G G G T C C C    A A G G G A A A A A
99-1 7001-13294  T T T A T G T A G T    T G G G G A T C T C    A A G G A A A G A A

                                4600                    4610                    4620
00-1 7001-13350  C A T T A A A G A T    G A A G A T A T A G    T A G A T G A A T C
99-1 7001-13294  T G T A A A A G A T    G A A G A T A T A A    T A G A T G A A T C

                                4630                    4640                    4650
00-1 7001-13350  A A T A G A T A A A    C T G T T A A G A G    T T G A T A A T A C
99-1 7001-13294  C A T T G A C A A A    T T A T T A A G A A    T T G A C A A C A C

                                4660                    4670                    4680
00-1 7001-13350  T T T T T G G A G A    A T G T T C A G C A    A G G T T A T G T T
99-1 7001-13294  C T T T T G G A G A    A T G T T C A G C A    A A G T C A T G T T
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Figure 53 cont'd

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                              4690                    4700                   4710
00-1 7001-13350  T G A A T C A A A G    G T T A A G A A A A    G G A T A A T G T T
99-1 7001-13294  T G A A T C A A A A    G T C A A A A A A A    G A A T A A T G T T

                              4720                    4730                   4740
00-1 7001-13350  A T A T G A T G T A    A A A T T T C T A T    C A T T A G T A G G
99-1 7001-13294  A T A T G A T G T G    A A A T T C C T A T    C A T T A G T A G G

                              4750                    4760                   4770
00-1 7001-13350  T T A T A T A G G G    T T T A A G A A T T    G G T T T A T A G A
99-1 7001-13294  T T A T A T A G G A    T T T A A A A A C T    G G T T T A T A G A

                              4780                    4790                   4800
00-1 7001-13350  A C A G T T G A G A    T C A G C T G A G T    T G C A T G A G G T
99-1 7001-13294  A C A G T T A A G A    G T G G T A G A A T    T G C A T G A G G T

                              4810                    4820                   4830
00-1 7001-13350  A C C T T G G A T T    G T C A A T G C C G    A A G G T G A T C T
99-1 7001-13294  A C C T T G G A T T    G T C A A T G C T G    A A G G A G A G T T

                              4840                    4850                   4860
00-1 7001-13350  G G T T G A G A T C    A A G T C A A T T A    A A A T C T A T T T
99-1 7001-13294  A G T T G A A A T T    A A A T C A A T C A    A A A T T T A T C T

                              4870                    4880                   4890
00-1 7001-13350  G C A A C T G A T A    G A G C A A A G T T    T A T T T T T A A G
99-1 7001-13294  G C A G T T A A T A    G A A C A A A G T C    T A T C T T T G A G

                              4900                    4910                   4920
00-1 7001-13350  A A T A A C T G T T    T T G A A C T A T A    C A G A T A T G G C
99-1 7001-13294  A A T A A C T G T A    T T G A A T T A T A    C A G A C A T G G C

                              4930                    4940                   4950
00-1 7001-13350  A C A T G C T C T C    A C A A G A T T A A    T C A G A A A G A A
99-1 7001-13294  A C A T G C T C T T    A C A C G A T T A A    T T A G G A G A A A

                              4960                    4970                   4980
00-1 7001-13350  G T T G A T G T G T    G A T A A T G C A C    T A T T A A C T C C
99-1 7001-13294  A T T G A T G T G T    G A T A A T G C A C    T C T T T A A T C C

                              4990                    5000                   5010
00-1 7001-13350  G A T T C C A T C C    C C A A T G G T T A    A T T A A C T C A
99-1 7001-13294  A A G T T C A T C A    C C A A T G T T T A    A T C T A A C T C A

                              5020                    5030                   5040
00-1 7001-13350  A G T T A T T G A T    C T C A C A G A A C    A A T T A G A C T T A
99-1 7001-13294  G G T T A T T G A T    C C C A C A A C A C    A A C T A G C T T A

                              5050                    5060                   5070
00-1 7001-13350  T T T C C C T A A G    A T A A C A T T T G    A A A G G C T A A A
99-1 7001-13294  T T T T C C T A G G    A T A A T A T T T G    A G A G G T T A A A
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Figure 53 cont'd

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                          5080                    5090                    5100
00-1 7001-13350  A A A T T A T G A C    A C T A G T T C A A    A T T A T G C T A A
99-1 7001-13294  A A G T T A T G A T    A C C A G T T C A G    A C T A C A A C A A

                          5110                    5120                    5130
00-1 7001-13350  A G G A A A G C T A    A C A A G G A A T T    A C A T G A T A C T
99-1 7001-13294  A G G G A A G T T A    A C A A G G A A T T    A C A T G A C A T T

                          5140                    5150                    5160
00-1 7001-13350  G T T G C C A T G G    C A A C A T G T T A    A T A G A T A T A A
99-1 7001-13294  A T T A C C A T G G    C A A C A C G T A A    A C A G G T A C A A

                          5170                    5180                    5190
00-1 7001-13350  C T T T G T C T T T    A G T T C T A C T G    G A T G T A A A G T
99-1 7001-13294  T T T T G T C T T T    A G T T C T A C A G    G T T G T A A A G T

                          5200                    5210                    5220
00-1 7001-13350  T A G T C T A A A A    A C A T G C A T T G    G A A A C T T A T
99-1 7001-13294  C A G T T T G A A G    A C A T G C A T C G    G G A A A T T G A T

                          5230                    5240                    5250
00-1 7001-13350  G A A A G A T C T A    A A C C C T A A A G    T T C T G T A C T T
99-1 7001-13294  A A A G G A T T T A    A A T C C T A A A G    T T C T T T A C T T

                          5260                    5270                    5280
00-1 7001-13350  T A T T G G A G A A    G G G G C A G G A A    A T T G G A T G G C
99-1 7001-13294  T A T T G G A G A A    G G A G C A G G T A    A C T G G A T G G C

                          5290                    5300                    5310
00-1 7001-13350  C A G A A C A G C A    T G T G A A T A T C    C T G A C A T C A A
99-1 7001-13294  A A G A A C A G C A    T G T G A A T A T C    C T G A T A T A A A

                          5320                    5330                    5340
00-1 7001-13350  A T T T G T A T A C    A G A G T T T A A    A A G A T G A C C T
99-1 7001-13294  A T T T G T A T A T    A G G A G T T T A A    A G G A T G A C C T

                          5350                    5360                    5370
00-1 7001-13350  T G A T C A T C A T    T A T C C T T T G G    A A T A C C A G A G
99-1 7001-13294  T G A T C A C C A T    T A C C C A T T A G    A A T A T C A A A G

                          5380                    5390                    5400
00-1 7001-13350  A G T T A T A G G A    G A A T T A A G C A    G G A T A A T A G A
99-1 7001-13294  G G T A A T A G G T    G A T C T A A A T A    G G G T G A T A G A

                          5410                    5420                    5430
00-1 7001-13350  T A G C G G T G A A    G G G C T T T C A A    T G G A A A C A A C
99-1 7001-13294  T A G T G G T G A A    G G A T T A T C A A    T G G A A A C A A C

                          5440                    5450                    5460
00-1 7001-13350  A G A T G C A A C T    C A A A A A A C T C    A T T G G G A T T T
99-1 7001-13294  A G A T G C A A C T    C A A A A A A C T C    A T T G G G A C T T
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Figure 53 cont'd

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                                  5470              5480              5490
00-1 7001-13350  G A T A C A C A G A   G T A A G C A A A G   A T G C T T T A T T
99-1 7001-13294  G A T A C A C A G A   A T A A G T A A A G   A T G C T T T A T T

                                  5500              5510              5520
00-1 7001-13350  A A T A A C T T T A   T G T G A T G C A G   A A T T T A A G G A
99-1 7001-13294  G A T A A C A T T G   T G T G A T G C A G   A A T T C A A A A A

                                  5530              5540              5550
00-1 7001-13350  C A G A G A T G A T   T T T T T A A G A   T G G T A A T T C T
99-1 7001-13294  C A G A G A T G A T   T T C T T T A A G A   T G G T A A T T C T

                                  5560              5570              5580
00-1 7001-13350  A T G G A G G A A A   C A T G T A T T A T   C A T G C A G A A T
99-1 7001-13294  T T G G A G A A A A   C A T G T A T T A T   C A T G G A G A A T

                                  5590              5600              5610
00-1 7001-13350  T T G C A C T A C T   T A T G G G A C A G   A C C T C T A T T T
99-1 7001-13294  C T G T A C A G C T   T A T G G G A C A G   A T C T T T A C T T

                                  5620              5630              5640
00-1 7001-13350  A T T C G C A A A G   T A T C A T G C T A   A A G A C T G C A A
99-1 7001-13294  A T T T G C A A A G   T A T C A T C G G   T G G A C T G C A A

                                  5650              5660              5670
00-1 7001-13350  T G T A A A A T T A   C C T T T T T T T G   T G A G A T C A G T
99-1 7001-13294  T A T A A A A T T A   C C A T T T T T T G   T A A G A T C T G T

                                  5680              5690              5700
00-1 7001-13350  A G C C A C C T T T   A T T A T G C A A G   G T A G T A A A C T
99-1 7001-13294  A G C T A C T T T T   A T T A T G C A A G   G A A G C A A A T T

                                  5710              5720              5730
00-1 7001-13350  G T C A G G C T C A   G A A T G C T A C A   T A C T T C T T A A C
99-1 7001-13294  A T C A G G G T C A   G A A T G C T A C A   T A C T T T T A A C

                                  5740              5750              5760
00-1 7001-13350  A C T A G G C C A C   C A C A A C A A T T   T A C C C T G C C A
99-1 7001-13294  A T T A G G T C A T   C A C A A T A A T C   T A C C C T G T C A

                                  5770              5780              5790
00-1 7001-13350  T G G A G A A A T   C A A A A T T C T A   A G A T G A A A A T
99-1 7001-13294  T G G A G A A A T A   C A A A A T T C C A   A A A T G A G A A T

                                  5800              5810              5820
00-1 7001-13350  A G C A G T G T G T   A A T G A T T T T T   A T G C T G C A A A
99-1 7001-13294  A G C A G T G T G T   A A T G A T T T C T   A T G C C T C A A A

                                  5830              5840              5850
00-1 7001-13350  A A A C T T G A C   A A T A A A T C T A   T T G A A G C C A A
99-1 7001-13294  G A A A C T G G A C   A A C A A A T C A A   T T G A A G C A A A
```

Figure 53 cont'd

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                          5860            5870            5880
00-1 7001-13350  C T G T A A A T C A   C T T T T A T C A G   G G C T A A G A A T
99-1 7001-13294  C T G C A A A T C T   C T T C T A T C A G   G A T T G A G A A T

                          5890            5900            5910
00-1 7001-13350  A C C G A T A A A T   A A G A A A G A A T   T A A A T A G A C A
99-1 7001-13294  A C C T A T A A A C   A A A A A G G A G T   T A A A T A G A C A

                          5920            5930            5940
00-1 7001-13350  G A G A A G G T T A   T T A A C A G T T G   A A A G C A A C C A
99-1 7001-13294  A A A G A A A T T G   T T A A C A C T A C   A A A G T A A C C A

                          5950            5960            5970
00-1 7001-13350  T T C T T C T G T A   G C A A C A G T T G   G A G G T A G C A A
99-1 7001-13294  T T C T T C T A T A   G C A A C A G T T G   G C G G C A G T A A

                          5980            5990            6000
00-1 7001-13350  G G T C A T A G A G   T C T A A A T G G T   T A A C A A A C A A
99-1 7001-13294  G A T T A T A G A A   T C C A A A T G G T   T A A A G A G A A T

                          6010            6020            6030
00-1 7001-13350  G G C A A A C A C A   A T A A T T G A T T   G G T T A G A A C A
99-1 7001-13294  A G C A A G T A C A   A T A A T T G A T T   G G T T A G A G C A

                          6040            6050            6060
00-1 7001-13350  T A T T T T A A A T   T C T C C A A A A G   G T G A A T T A A A
99-1 7001-13294  T A T T T T G A A T   T C T C C A A A A G   G T G A A T T A A A

                          6070            6080            6090
00-1 7001-13350  T T A T G A T T T T   T T T G A A G C A T   T A G A A A A T A C
99-1 7001-13294  C T A T G A T T T C   T T T G A A G C A T   T A G A G A A C A C

                          6100            6110            6120
00-1 7001-13350  T T A C C C T A A T   A T G A T T A A A C   T A A T A G A T A A
99-1 7001-13294  A T A C C C A A T    A T G A T C A A G C   T T A T A G A T A A

                          6130            6140            6150
00-1 7001-13350  T C T A G G G A A T   G C A G A G A T A A   A A A A A C T G A T
99-1 7001-13294  T T T G G G A A T    G C A G A A A T A A   A G A A A C T A A T

                          6160            6170            6180
00-1 7001-13350  C A A G T A A C T    G G A T A T A T G C   T T G T A G A C A
99-1 7001-13294  C A A G G T C A C T   G G G T A T A T G C   T T G T G A G T A A

                          6190            6200            6210
00-1 7001-13350  A A A A T G A A A T   A T G A T A A A A    T C A T A A A A T A
99-1 7001-13294  G A A G T - A A T A   A T A A T G A T A A   T G A T T A A C C A

                          6220            6230            6240
00-1 7001-13350  G G T G A C A A C T   T C A T A C T A T T   C C - A A A G T A A
99-1 7001-13294  - - - - - T A A T C   T C A C A C A A C T   G A G A A A A T A A
```

Figure 53 cont'd

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                               6250                      6260              6270
0-1 7001-13350  T C A T T T G A T T   A T G C A A T T A T   G T A A T A G T T A
9-1 7001-13294  T C G T C T A A C A   G T T T A G T T G A   T C A T T A G T T A

                               6280                      6290              6300
0-1 7001-13350  A T T A A A A C T   A A A A A T C A A A   A G T T A G A A A C
9-1 7001-13294  T T T A A A A T T A   T A A A A T A G T A   A C T A A C T G A T

                               6310                      6320              6330
0-1 7001-13350  T A A C A A C T G T   C A T T A A G T T T   A T T A A A A A T A
9-1 7001-13294  A A A A A T C A G   A A A T T G A A A T   T G A A T G T A T A

                               6340                      6350              6360
0-1 7001-13350  A G A A T T A T A   A T T G G A T G T A   T A C G
9-1 7001-13294  C G G T T T T T T T   G C C G T
```

Figure 53 cont'd

FIGURE 54

APPROACHES

A. Self Ligation

vRNA (-)

PPP ——— → TAP

P ———

→ RNA Ligase

→ RT-PCR/ Nested PCR

Junction Frag.

B. 3' RACE

vRNA (-)

PPP ——— → PolyA polymerase

PPP ——— (A)n

→ RT-PCR/ Nested PCR

C. 5' RACE

vRNA (-)

PPP ——— → TAP

3' OH P ———
RNA Oligo

→ RNA Ligase

→ RT-PCR/ Nested PCR
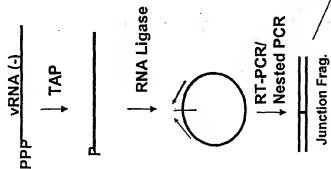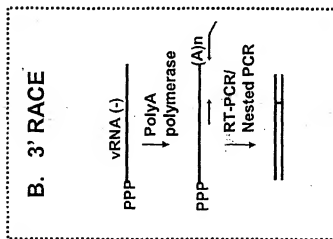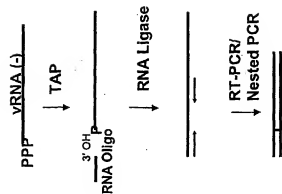
Consensus Sequence Analysis or Clonal Sequence Analysis

FIGURE 55

5' cDNA Terminal Sequences of hMPV

Poly A Track

A? C? G?
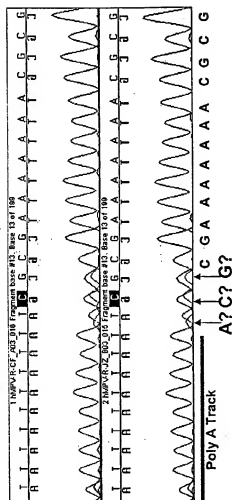
Clonal Analysis of 96 PCR colonies

	# Colony	Ratio
5'-ACGCGAAAAAACGCG	15	31%
CGCGAAAAAAACGCG	6	12%
GCGAAAAAAACGCG	5	10%
CGAAAAAAACGCG	23	47%

Total 49 near full-length clones

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SEQUENCE LISTING

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     ViroNovative BV

<120> METAPNEUMOVIRUS STRAINS AND THEIR
     USE IN VACCINE FORMULATIONS AND AS
     VECTORS FOR EXPRESSION OF
     ANTIGENIC SEQUENCES

<130> 7682-063-228

<140> To be assigned
<141> Herewith

<160> 389

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<223> Human metapneumovirus isolate 00-1 matrix protein
     (M) and fusion protein (F) genes

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ttggtagcct gttatgacgg tatgagttgt tccattggaa gcaacaaggt tggaataatc 1200
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gacaacacag tgtaccaatt gagcaaagtt gaaggagaac aacacacaat taaagggaag 1320
ccagtcatca gcaatcttga ccctataggg ttccctgaag atcagttcaa cgtagcccctg 1380
gatcaggtgt ttgaaagtgt tgagaaggat cagaatctga tagaccagtc aaacaagata 1440
ttggatagca ttgaaaaggg gaatgcagga tttgtcatag tgatagtcct cattgtcctg 1500
ctcatgctgg cagcagtttg tgtgggtgtc ttctttgtgg ttaagaagag aaaagctgct 1560
cccaaattcc caatggtgaaat gaatggtgtg aacaac 1596
```

<210> 3
<211> 1666
<212> DNA
<213> pneumovirus

<220>
<221> CDS
<222> (14)...(1627)
<223> Avian pneumovirus isolate lb fusion protein mRNA,

2

complete cds

<400> 3
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gggacaagtg aaaatgtctt ggaaagtggt actgctattg gtattgctag ctaccccaac    60
gggtggggcta gaagaaagtt atctagagga gtcatgcagt actgttacta gaggataact   120
gagtgtttttg aggacaggat ggtatacaaa tgtgttcaca cttgaggttg gagatgtgga   180
aaatctcaca tgtaccgacg ggcccagctt aataagaaca gaacttgaac tgacaaaaaa   240
tgcacttgag gaactcaaga cagtatcagc agatcaattg gcaaaggaag ctaggataat   300
gtcaccaaga aaagcccggt ttgttctggg tgccatagca ttaggtgtgg caactgctgc   360
tgctgtgaca gctggtgtag cgatagccaa gacaattagg ctagaaggag aagtggctgc   420
aatcaaggt gcgctcagga aaacaaatga ggctgtatct acattaggaa atggcgtgag   480
ggtacttgca acagctgtga atgatctcaa ggactttata agtaaaaaat tgacacctac   540
aataaacagg aacaagtgtg acatctcaga ccttaagatg gcagtgagct ttggacaata   600
caatcggagg ttcctcaatg tggtaagaca gttttctgac aatgcaggta ttacgcctgc   660
aatatctcta gatttaatga ctgacgctga gcttgtaaga gctgtaagca acatgcccac   720
atcttcagga cagatcaatc tgatgcttga gaatcgggca atgtcagaa ggaaaggatt   780
tgggattttg attggagttt atggtagctc tgtggtctat atagtgcagc ttctcatttt   840
cggtgtgata gatacacctgt gttggaaggt gaaggctgct ccattatgtt cagggaaaga   900
cgggaattat gcatgtctct tgcgagagga ccaaggttgg tattgtcaaa atgctggatc   960
cacagtttat tatccaaatg aggaggactg tgaagtaaga agtgatcatg tgtttgtga   1020
cacagcagct gggataaatg tagcaaagga gtcagaagag tgcaacagga atatctcaac   1080
aacaaagtac ccttgcaagg taagtacagg gcgtcaccca ataagcatgg tggccttatc   1140
accactgggt gctttggtag cctgttatga cggtatgagt tgttccattg gaagcaacaa   1200
ggttggaata atcagacctt tgggggaaagg gtgttcatac atcagcaatc aagatgctga   1260
cactgttaca attgacaaca cagtgtacca attgagcaaa gttgaaggag aacaacacac   1320
aattaaaggg aagccagtat ctagcaattt tgaccctata gagttccctg aagatcagtt   1380
caacgtagcc ctggatcagg tgtttgaaag tgttgagaag agtcagaatc tgatagacca   1440
gtcaaacaag atattggata gcattgaaaa ggggaatgca ggatttgtca tagtgatagt   1500
cctcattgtc ctgctcatgc tggcagcagt tggtgtgggt gtcttctttg tggttaagaa   1560
gagaaaagct gctcccaaat tcccaatgga aatgaatggt gtgaacaaca aaggatttat   1620
cccttaattt tagttattaa aaaaaaaaaa aaaaaaaaaa aaaaaa                   1666
```

<210> 4
<211> 1636
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (13)...(1629)
<223> Turkey rhinotracheitis virus gene for fusion
      protein (F1 and F2 subunits), complete cds

<400> 4
```
gggacaagta ggatggatgt aagaatctgt ctcctattgt tccttatatc taatcctagt    60
agctgcatac aagaaaacata caatgaagaa tcctgcagta ctgtaactag aggttataag   120
agtgtgttaa ggacagggtg gtatacgaat gtatttaacc tcgaaatagg gaatgttgga   180
aacatcactt gcaatgatgg acccagccta attgacactg agttagtact cacaaagaat   240
gctttgaggg agctcaaaac agtgtcagct gatcaagtgg ctaaggaaag cagactatcc   300
tcacccagga gacgtagatt tgtactgggt gcaatagcac ttggtgttgc gacagctgct   360
gccgtaacag ctggtgtagc acttgcaaag acaattagat tagaggggga ggtgaaaggca   420
attaagaatg ccctccggaa cacaaatgag gcagtatcca cattagggaa tggtgtgagg   480
gtactagcaa ctgcagtcaa tgacctcaaa gaatttataa gtaaaaaatt gactcctcct   540
attaaccaga acaaatgcaa tatagcagat ataaagatgg caattagttt tggccaaaat   600
aacagaaggt tcctgaatgt ggtgaggcaa ttctctgata gtgcaggtat cacatcagct   660
gtgtctcttg atttaatgac agatgatgaa cttgttagag caattaacag aatgccaact   720
tcatcaggac agattagttt gatgttgaac aatcgtgcca tggttgaact cacatcatcc   780
ggtataatta ttggtgttta tgatgaacg gtcgtttata tgtacaact gcccatattc   840
gccgtggttg agacacctg ttggagggtg gtgcagcac cactcgttag gaaagagaaa   900
gggaattatg cttgtacact gagagaagat caagggtggt actgtacaaa tgctggctcc   960
acagtttatt atcctaataa agatgattgt gaggtaaggg atgattatgt atttgtgac   1020
acagcagctg gcattaatgt ggccctagaa gttgaacagt gcaactataa catatcgact   1080
```

3

```
tctaaatacc catgcaaagt cagcacaggt agacaccctg tcagtatggt agccttaacc 1140
cccctagggg gtctagtgtc ttgttatgag agtgtaagtt gctccatagg tagcaataaa 1200
gtagggataa taaaacagct aggcaaaggg tgcacccaca ttcccaacaa cgaagctgac 1260
acgtaaacca ttgataacac tgtgtaccaa ttgagcaagg ttgtaggcga acagaggacc 1320
ataaaaggag ctccagttgt gaacaatttt aacccaatat tattccctga ggatcagttc 1380
aatgttgcac ttgatcaagt atttgagagt atagatagat ctcagactt aataagataag 1440
tctaacgacc tgctaggtcg agatgccaag agcaaggctg gaattgctat agcaatagta 1500
gtgctagtca ttcttaggaat cttcttttta cttgcagtga tatattactg ttccagagtc 1560
cggaagacca aaccaaagca tgattacccg gccacgacag gtcatagcag catggcttat 1620
gtcagttaag ttattt                                                  1636
```

<210> 5
<211> 1860
<212> DNA
<213> pneumovirus

<220>
<221> CDS
<222> (1)...(110)
<223> Avian pneumovirus matrix protein (M) gene, partial
      cds

<220>
<221> CDS
<222> (216)...(1829)
<223> Avian pneumovirus fusion glycoprotein (F) gene,
      complete cds

```
<400> 5
gagttcaggt aatagtggag ttaggggcat acgttcaagc agaaagcata agcagaatct 60
gcaggaactg gagccaccag ggtacgagat atgtcctgaa gtcaagataa acacagagag 120
tacacttacc aaatcacagt aacaatttcg tttttaaccc tctcatagtt attacctagc 180
ttgatattat ttagaaaaaa tcgggacaag tgaaaatgtc ttggaaagtg gtactgctat 240
tgtgtattgct agctaccccca acgggggggc tagaagaaag ttatctagag gagtcatgca 300
gtactgttac tagaggatac ctgagtgttt tgaggacagg atggtataca aatgtgttca 360
cacttgaggt tggagatgtg gaaaatctca catgtaccga cgggcccagc ttaataagaa 420
cagaacttga actgacaaaa aatgccacttg aggaactcaa gacagtatca gcagatcaat 480
tggcaaagga agctaggata atgtcaccaa gaaaagcccg gtttgttctg cggtgccatag 540
cattaggtgt ggcaactgct gctgctgtga cggctggtgt agcgatagcc aagacaatta 600
ggctagaagg agaagtggct gcaatcaagg gtgcgctcag gaaaacaaat gggctgttat 660
ctacattagg aaatggcgtg agggtacttg caacagctgt gaatgatctc aaggactta 720
taagtaaaaa attgacacct gcaataaaca ggaacaagtg tgacatctca gaccttaaga 780
tggcagtgag ctttggacaa tacaatcgga ggttcctcaa tgtggtaaga cagtttttctg 840
acaatgcagg tattaccgct gcaatatctc tagatttaat gactgacgct gagcttgtaa 900
gagctgtaag caacatgccc acatcttcag gacagatcaa tctgatgctt gagaatcggg 960
caatggtcag aaggaaagta tttgggattt tgatttgagt ttatggtagc tctgtggtct 1020
atatagtgca gcttcctctt ttcggtgtga tagatacacc gtgttggaag gtgaaggggtc 1080
ctccattatg ttcagggaaa gacgggaatt atgcatgtct cttgcgagag gaccaaggtt 1140
ggtattgtca aaatgctgga tccaggtttt attatccaaa tgaggaggac tgtgaagtaa 1200
gaagtgatca tgtgttttgt gacacagcag ctgggataaa tgtagcaaag gagtcagaag 1260
agtgcaacag gaatatctca acaacaaagt acccttgcaa ggtaagtaca gggcgtcacc 1320
caataagcat ggtggcctta tcaccactgg gtgctttggt agcctgttat gacggttatga 1380
gttgttccat tggaagcaac aaggttggaa taatcagacc tttggggaaa gggtgttcat 1440
acatcagcaa tcaagatgct gacactgtta caattgacaa cacagtgtac caattgagca 1500
aagttgaagg agaacaacac acaattaaag ggaagccagt attctagcaat tttgaccct a 1560
tagagttccc tgaagatcag ttcaacatag ccctggatca ggtgtttgaa agtgttgaga 1620
agagtcagaa tctgatagac cagtcaaaca agatattgga tagcattgaa aagggggaata 1680
caggatttgt catagtgata gtcctcattg tcctgctcat gctggcagca gttggtgtgg 1740
gtgtctctt tgtggttaag aagagaaaag ctgctcccaa attcccaatg gaaatgaatg 1800
gtgtgaacaa caaaggattt atcccttaat tttagttact aaaaaattgg gacaagtgaa 1860
```

4

```
<210> 6
<211> 574
<212> PRT
<213> paramyxovirus

<220>
<223> paramyxovirus F protein hRSV B

<400> 6
Met Glu Leu Leu Ile His Arg Leu Ser Ala Ile Phe Leu Thr Leu Ala
 1               5                  10                  15
Ile Asn Ala Leu Tyr Leu Thr Ser Ser Gln Asn Ile Thr Glu Glu Phe
               20                  25                  30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Arg Gly Tyr Phe Ser Ala Leu
           35                  40                  45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
       50                  55                  60
Lys Glu Thr Lys Cys Asn Gly Thr Asp Thr Lys Val Lys Leu Ile Lys
65                  70                  75                  80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
               85                  90                  95
Met Gln Asn Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Ala Pro
               100                 105                 110
Gln Tyr Met Asn Tyr Thr Ile Asn Thr Thr Lys Asn Leu Asn Val Ser
           115                 120                 125
Ile Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
       130                 135                 140
Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145                 150                 155                 160
Glu Gly Glu Val Asn Lys Ile Lys Asn Ala Leu Leu Ser Thr Asn Lys
               165                 170                 175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
               180                 185                 190
Leu Asp Leu Lys Asn Tyr Ile Asn Asn Gln Leu Leu Pro Ile Val Asn
           195                 200                 205
Gln Gln Ser Cys Arg Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
       210                 215                 220
Gln Lys Asn Ser Arg Leu Leu Glu Ile Asn Arg Glu Phe Ser Val Asn
225                 230                 235                 240
Ala Gly Val Thr Thr Pro Leu Ser Thr Tyr Met Leu Thr Asn Ser Glu
               245                 250                 255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
               260                 265                 270
Leu Met Ser Ser Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
           275                 280                 285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
       290                 295                 300
Ile Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320
Leu Cys Thr Thr Asn Ile Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
               325                 330                 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
           340                 345                 350
Pro Gln Ala Asp Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
       355                 360                 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Ser Leu Cys Asn Thr
   370                 375                 380
Asp Ile Phe Asn Ser Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400
Asp Ile Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
               405                 410                 415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
```

5

```
                 420                      425                      430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
            435                      440                      445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Leu Glu Gly
    450                      455                      460
Lys Asn Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Tyr Tyr Asp Pro
465                      470                      475                      480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                    485                      490                      495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Arg Ser Asp Glu Leu
            500                      505                      510
Leu His Asn Val Asn Thr Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515                      520                      525
Thr Ile Ile Ile Val Ile Ile Val Val Leu Leu Ser Leu Ile Ala Ile
        530                      535                      540
Gly Leu Leu Leu Tyr Cys Lys Ala Lys Asn Thr Pro Val Thr Leu Ser
545                      550                      555                      560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Lys
                    565                      570


<210> 7
<211> 574
<212> PRT
<213> paramyxovirus

<220>
<223> paramyxovirus F protein hRSV A2

<400> 7
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1                   5                       10                      15
Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
                20                      25                      30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                      40                      45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                      55                      60
Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                      70                      75                      80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
                85                      90                      95
Met Gln Ser Thr Pro Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                     105                     110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                     120                     125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                     135                     140
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
145                     150                     155                     160
Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                     170                     175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
            180                     185                     190
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
        195                     200                     205
Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                     215                     220
Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                     230                     235                     240
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
```

6

```
                    245                      250                      255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
              260                      265                      270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
          275                      280                      285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
      290                      295                      300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                      310                      315                      320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                  325                      330                      335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
              340                      345                      350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
          355                      360                      365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn Val
      370                      375                      380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                      390                      395                      400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                  405                      410                      415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
              420                      425                      430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met Asp
          435                      440                      445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
      450                      455                      460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                      470                      475                      480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                  485                      490                      495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
              500                      505                      510
Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
          515                      520                      525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
      530                      535                      540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                      550                      555                      560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                  565                      570
```

```
<210> 8
<211> 121
<212> PRT
<213> metapneumovirus

<220>
<223> human metapneumovirus01-71 (partial sequence)

<400> 8
Leu Leu Ile Thr Pro Gln His Gly Leu Lys Glu Ser Tyr Leu Glu Glu
 1               5                      10                      15
Ser Cys Ser Thr Ile Thr Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly
              20                      25                      30
Trp Tyr Thr Asn Val Phe Thr Leu Glu Val Gly Asp Val Glu Asn Leu
          35                      40                      45

Thr Cys Ala Asp Gly Pro Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr
      50                      55                      60
Lys Ser Ala Leu Arg Glu Leu Arg Thr Val Ser Ala Asp Gln Leu Ala
```

7

```
65                    70                    75                    80
Arg Glu Glu Gln Ile Glu Asn Pro Arg Gln Ser Arg Phe Val Leu Gly
                          85                    90                    95
Ala Ile Ala Leu Gly Val Ala Thr Ala Ala Ala Val Thr Ala Gly Val
                100                   105                   110
Ala Ile Ala Lys Thr Ile Arg Leu Glu
            115                   120
```

```
<210> 9
<211> 539
<212> PRT
<213> metapneumovirus

<220>
<223> Human metapneumovirus isolate 00-1 matrix protein
      (M) and fusion protein (F) genes

<400> 9
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1                     5                     10                    15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
                20                    25                    30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                    40                    45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
50                    55                    60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                    70                    75                    80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                    90                    95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
                100                   105                   110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
            115                   120                   125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
        130                   135                   140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                   150                   155                   160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                   170                   175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
            180                   185                   190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                   200                   205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210                   215                   220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                   230                   235                   240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                   250                   255
Gly Phe Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                   265                   270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                   280                   285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
        290                   295                   300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                   310                   315                   320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                   330                   335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
```

8

```
                 340                        345                     350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
             355                  360                    365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370                    375                    380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                    390                    395                    400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                    405                    410                    415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
             420                    425                    430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
      435                    440                    445
Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
      450                    455                    460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                    470                    475                    480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
             485                    490                    495
Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
      500                    505                    510
Ile Ile Lys Lys Thr Lys Arg Pro Thr Gly Ala Pro Pro Glu Leu Ser
      515                    520                    525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
      530                    535

<210> 10
<211> 532
<212> PRT
<213> Avian pneumovirus

<220>
<223> Avian pneumovirus fusion protein gene, partial cds

<400> 10
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
1                 5                      10                     15
Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
             20                     25                     30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35                     40                     45
Thr Leu Gly Val Gly Asp Val Lys Asn Leu Thr Cys Thr Asp Gly Pro
50                     55                     60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
65                     70                     75                     80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
             85                     90                     95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
             100                    105                    110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
      115                    120                    125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
      130                    135                    140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                    150                    155                    160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
             165                    170                    175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
      180                    185                    190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
      195                    200                    205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
```
                                          9

```
     210                    215                    220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
225                    230                    235                    240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                    250                    255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
                260                    265                    270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Arg Val Lys Ala
        275                    280                    285
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
        290                    295                    300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                    310                    315                    320
Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
                325                    330                    335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
                340                    345                    350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                    360                    365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
        370                    375                    380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385                    390                    395                    400
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
                405                    410                    415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
        420                    425                    430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
        435                    440                    445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
450                    455                    460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
465                    470                    475                    480
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
        485                    490                    495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
        500                    505                    510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
        515                    520                    525
Gly Val Asn Asn
        530
```

```
<210> 11
<211> 537
<212> PRT
<213> Avian pneumovirus

<220>
<223> Avian pneumovirus isolate 1b fusion protein mRNA,
      complete cds

<400> 11
```

```
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
1                    5                    10                    15
Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
                20                    25                    30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                    40                    45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
50                    55                    60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
65                    70                    75                    80
```

```
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
                85                      90                  95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
                165                 170                 175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
            180                 185                 190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
225                 230                 235                 240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
            260                 265                 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
        275                 280                 285
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320
Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
            340                 345                 350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
            355                 360                 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
        370                 375                 380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385                 390                 395                 400
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Gln Leu Ser Lys Val Glu Gly Ala Asp Ile
                405                 410                 415
Thr Val Thr Ile Gly Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
            420                 425                 430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
        435                 440                 445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
465                 470                 475                 480
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
                485                 490                 495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
            500                 505                 510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
        515                 520                 525
Gly Val Asn Asn Lys Gly Phe Ile Pro
    530                 535
        .
<210> 12
<211> 538
```

```
<212> PRT
<213> Turkey rhinotracheitis virus

<220>
<223> Turkey rhinotracheitis virus gene for fusion
      protein (F1 and F2 subunits), complete cds

<400> 12
Met Asp Val Arg Ile Cys Leu Leu Leu Phe Leu Ile Ser Asn Pro Ser
1               5                   10                  15
Ser Cys Ile Gln Glu Thr Tyr Asn Glu Glu Ser Cys Ser Thr Val Thr
            20                  25                  30
Arg Gly Tyr Lys Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
Asn Leu Glu Ile Gly Asn Val Glu Asn Ile Thr Cys Asn Asp Gly Pro
    50                  55                  60
Ser Leu Ile Asp Thr Gly Leu Val Leu Thr Lys Asn Ala Leu Arg Glu
65                  70                  75                  80
Leu Lys Thr Val Ser Ala Asp Gln Val Ala Lys Glu Ser Arg Leu Ser
                85                  90                  95
Ser Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Leu Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Gly Glu Val Lys Ala Ile Lys Asn Ala Leu Arg Asn Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Asn Asp Leu Lys Glu Phe Ile Ser Lys Leu Ser Leu Thr Pro Ala
                165                 170                 175
Ile Asn Gln Asn Lys Cys Asn Ile Ala Asp Ile Lys Met Ala Ile Ser
            180                 185                 190
Phe Gly Gln Asn Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Ser Ala Gly Ile Thr Ser Ala Val Ser Leu Asp Leu Met Thr Asp
210                 215                 220
Asp Glu Leu Val Arg Ala Ile Asn Arg Met Pro Thr Ser Ser Gly Gln
225                 230                 235                 240
Ile Ser Leu Met Leu Asn Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Asp Gly Thr Val Val Tyr Met Val Gln
            260                 265                 270
Leu Pro Ile Phe Gly Val Ile Glu Thr Pro Cys Trp Arg Val Val Ala
        275                 280                 285
Ala Pro Leu Cys Arg Lys Gln Lys Gly Asn Tyr Ala Cys Ile Leu Arg
    290                 295                 300
Glu Asp Gln Gly Trp Tyr Cys Thr Asn Ala Gly Ser Thr Ala Tyr Tyr
305                 310                 315                 320
Pro Asn Lys Asp Asp Cys Glu Val Arg Asp Asp Tyr Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Leu Glu Val Glu Gln Cys Asn Tyr
            340                 345                 350
Asn Ile Ser Thr Ser Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365
Pro Val Ser Met Val Ala Leu Thr Pro Leu Gly Gly Leu Val Ser Cys
    370                 375                 380
Tyr Glu Ser Val Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385                 390                 395                 400
Lys Gln Leu Gly Lys Gly Cys Thr His Ile Pro Asn Asn Glu Ala Asp
                405                 410                 415
Thr Ile Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Val Gly
            420                 425                 430
```

```
Glu Gln Arg Thr Ile Lys Gly Ala Pro Val Val Asn Asn Phe Asn Pro
        435                 440                 445
Ile Leu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460
Glu Ser Ile Asp Arg Ser Gln Asp Leu Ile Asp Lys Ser Asn Asp Leu
465                 470                 475                 480
Leu Gly Ala Ala Ala Lys Ser Lys Ala Gly Ile Ala Ile Ala Ile Val
                485                 490                 495
Val Leu Val Ile Leu Gly Ile Phe Phe Leu Leu Ala Val Ile Tyr Tyr
            500                 505                 510
Cys Ser Arg Val Arg Lys Thr Lys Pro Lys His Asp Tyr Pro Ala Thr
        515                 520                 525
Thr Gly His Ser Ser Met Ala Tyr Val Ser
        530                 535
```

```
<210> 13
<211> 537
<212> PRT
<213> Avian penumovirus

<220>
<223> Avian pneumovirus fusion glycoprotein (F) gene,
      complete cds

<400> 13
```

```
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
 1               5                   10                  15
Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
                20                  25                  30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
    50                  55                  60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
65                  70                  75                  80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
                85                  90                  95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
                165                 170                 175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
            180                 185                 190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
225                 230                 235                 240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
            260                 265                 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
        275                 280                 285
```

13

```
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
    290                     295                 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                     310                 315                 320

Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
            340                 345                 350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365
Pro Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385                 390                 395                 400
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
            405                 410                 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
        420                 425                 430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
    435                 440                 445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Ile Ala Leu Asp Gln Val Phe
450                 455                 460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
465                 470                 475                 480
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
            485                 490                 495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
        500                 505                 510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
    515                 520                 525
Gly Val Asn Asn Lys Gly Phe Ile Pro
    530                 535
```

```
<210> 14
<211> 1193
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16)...(1191)
<223> Turkey rhinotracheitis virus (strain CVL14/1)
      attachment protien (G) mRNA, complete cds

<400> 14
gggacaagta tctctatggg gtccaaacta tatatggctc agggcaccag tgcatatcaa  60
actgcagtgg ggttctggct ggacatcggg aggaggtaca tattggctat agtcctatca 120
gctttcgggc tgacctgcac agtcactatt gcactcactg ttagcgtcat agttgaacag 180
tcagtgttag aggagtgcag aaactacaat ggaggagata gagattggtg gtcaaccacc 240
caggagcagc caactactgc accaagtgcg actccagcag gaaattatgg aggattacaa 300
acggctcgaa caagaaagtc tgaaagctgt ttgcatgtgc aaatttctta tggtgatatg 360
tatagccgca gtgatactgt actgggtggt tttgattgta tgggcttatt ggttctttgc 420
aaatcaggac caatttgtca gcgagataat caagttgacc caacagccct ctgccattgc 480
agggtagatc tttcaagtgt ggactggctg caaggtgaaca agattagcac taacagcgac 540
accacctctg agcccagaa gaccaacccg gcatggccta gccaagacaa cacagactgc 600
gatccaaatc cccaaggcat aaccaccagc acagccactc tgctctcaac aagtctgggc 660
ctcatgtctca catcgaagac tgggacacac aaatcaggc gcccccacaaa cttgccgggg 720
agcaacacca acggaaaaac aaccaccagc cgagaaccag ggccccacaa ccaaccaaat 780
tcaaccacca atgggcaaaca caataaacac acccaacgaa tgacaccccc gccaagtcac 840
gacaacacaa gaaccatcct ccagcacaca acacctgg aaaagacatt cagtacatac 900
aagcccacac actctccgac caacgaatca gatcaatccc tccccacaac tcaaaacagc 960
```

14

```
atcaactgtg aacattttga cccccaaggc aaggaaaaaa tctgctacag agtaggttct 1020
tacaactcca atattacaaa gcaatgcaga attgatgtgc ctttgtgttc cacttatagc 1080
acagtgtgca tgaaaacata ctataccgaa ccattcaact gttggaggcg tatctggcgt 1140
tgcttgtgtg atgacggagt tggtctggtt gagtggtgtt gcactagtta act         1193
```

<210> 15
<211> 1260
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16)...(1260)
<223> Turkey rhinotracheitis virus (strain 6574)
       attachment protein (G), complete cds

```
<400> 15
gggacaagta tccagatggg gtcagagctc tacatcatag aggggggtgag ctcatctgaa 60
atagtcctca agcaagtcct cagaaggagc caaaaaatac tgttaggact ggtgttatca 120
gccttaggct tgacgctcac tagcactatt gttatatcta tttgtattag tgtagaacag 180
gtcaaattac gacagtgtgt ggacacttat tgggcggaaa atggatcctt acatccagga 240
cagtcaacag aaaatacttc aacaagaggt aagactacaa caaaagaccc tagaagatta 300
caggcgactg gagcaggaaa gtttgagagc tgtgggtatg tgcaagttgt tgatggtgat 360
atgcatgatc gcagttatgc tgtactgggt ggtgttgatt gtttgggctt attggctctt 420
tgtgaatcag gaccaattg tcagggagat acttggtctg aagacggaaa cttctgccga 480
tgcacttttt cttcccatgg ggtgagttgc tgcaaaaaac ccaaaagcaa ggcaaccact 540
gcccagagga actccaaacc agctaacagc aaatcaactc ctccggtaca ttcagacagg 600
gccagcaaag aacataatcc ctcccaaggg gagcaacccc gcaggggggcc aaccagcagc 660
aagacaacta ttgctagcac cccttcaaca gaggacactg ctaaaccaac gattagcaaa 720
cctaaactca ccatcaggcc ctcgcaaaga ggtccatccg gcagcacaaa agcagcctcc 780
agcaccccca gccacaagac caacaccaga ggcaccagca agacgaccga ccagagaaccc 840
cgcaccggac ccactcccga aaggcccaga caaacccaca gcacagcaac tccgcccccc 900
acaaccccaa tccacaaggg ccgggcccca accccaaac caacaacaga cctcaaggtc 960
aacccaaggg aaggcagcac aagcccaact gcaatacaga aaaacccaac cacacaaagt 1020
aatcttgttg actgcacact gtctgatcca gatgagccac aaaggatttg ttaccaggta 1080
ggaacttaca atcctagtca atcgggaacc tgcaacatag aggttccaaa atgttccact 1140
tatgggcatg cttgtatggc tacattatat gacaccccat tcaactgctg gcgcaggacc 1200
aggagatgca tctgtgattc cggaggggag ctgattgagt ggtgctgtac tagtcaataa 1260
```

<210> 16
<211> 391
<212> PRT
<213> Turkey rhinotracheitis virus

<220>
<223> Turkey rhinotracheitis virus (strain CVL14/1)
       attachment protien (G) mRNA, complete cds

```
<400> 16
Met Gly Ser Lys Leu Tyr Met Ala Gln Gly Thr Ser Ala Tyr Gln Thr
1               5                   10                  15
Ala Val Gly Phe Trp Leu Asp Ile Gly Arg Arg Tyr Ile Leu Ala Ile
            20                  25                  30
Val Leu Ser Ala Phe Gly Leu Thr Cys Thr Val Thr Ile Ala Leu Thr
        35                  40                  45
Val Ser Val Ile Val Glu Gln Ser Val Leu Glu Glu Cys Arg Asn Tyr
    50                  55                  60
Asn Gly Gly Asp Arg Asp Trp Trp Ser Thr Thr Gln Glu Gln Pro Thr
65                  70                  75                  80
Thr Ala Pro Ser Ala Thr Pro Ala Gly Asn Tyr Gly Gly Leu Gln Thr
                85                  90                  95
Ala Arg Thr Arg Lys Ser Glu Ser Cys Leu His Val Gln Ile Ser Tyr
```

```
                  100                    105                   110
Gly Asp Met Tyr Ser Arg Ser Asp Thr Val Leu Gly Gly Phe Asp Cys
        115                    120                   125
Met Gly Leu Leu Val Leu Cys Lys Ser Gly Pro Ile Cys Gln Arg Asp
    130                    135                   140
Asn Gln Val Asp Pro Thr Ala Leu Cys His Cys Arg Val Asp Leu Ser
145                    150                   155                   160
Ser Val Asp Cys Cys Lys Val Asn Lys Ile Ser Thr Asn Ser Ser Thr
                  165                    170                   175
Thr Ser Glu Pro Gln Lys Thr Asn Pro Ala Trp Pro Ser Gln Asp Asn
        180                    185                   190
Thr Asp Ser Asp Pro Asn Pro Gln Gly Ile Thr Thr Ser Thr Ala Thr
        195                    200                   205
Leu Leu Ser Thr Ser Leu Gly Leu Met Leu Thr Ser Lys Thr Gly Thr
    210                    215                   220
His Lys Ser Gly Pro Pro Gln Ala Leu Pro Gly Ser Asn Thr Asn Gly
225                    230                   235                   240
Lys Thr Thr Thr Asp Arg Glu Pro Gly Pro Thr Asn Gln Pro Asn Ser
                  245                    250                   255
Thr Thr Asn Gly Gln His Asn Lys His Thr Gln Arg Met Thr Pro Pro
        260                    265                   270
Pro Ser His Asp Asn Thr Arg Thr Ile Leu Gln His Thr Thr Pro Trp
        275                    280                   285
Glu Lys Thr Phe Ser Thr Tyr Lys Pro Thr His Ser Pro Thr Asn Glu
    290                    295                   300
Ser Asp Gln Ser Leu Pro Thr Thr Gln Asn Ser Ile Asn Cys Glu His
305                    310                   315                   320
Phe Asp Pro Gln Gly Lys Glu Lys Ile Cys Tyr Arg Val Gly Ser Tyr
                  325                    330                   335
Asn Ser Asn Ile Thr Lys Gln Cys Arg Ile Asp Val Pro Leu Cys Ser
        340                    345                   350
Thr Tyr Ser Thr Val Cys Met Lys Thr Tyr Tyr Thr Glu Pro Phe Asn
        355                    360                   365
Cys Trp Arg Arg Ile Trp Arg Cys Leu Cys Asp Asp Gly Val Gly Leu
    370                    375                   380
Val Glu Trp Cys Cys Thr Ser
385                    390


<210> 17
<211> 414
<212> PRT
<213> rhinotracheitis virus

<220>
<223> Turkey rhinotracheitis virus (strain 6574)
      attachment protein (G), complete cds

<400> 17
Met Gly Ser Glu Leu Tyr Ile Ile Glu Gly Val Ser Ser Ser Glu Ile
1                   5                     10                   15
Val Leu Lys Gln Val Leu Arg Arg Ser Gln Lys Ile Leu Leu Gly Leu
            20                     25                   30
Val Leu Ser Ala Leu Gly Leu Thr Leu Thr Ser Thr Ile Val Ile Ser
        35                     40                   45
Ile Cys Ile Ser Val Glu Gln Val Lys Leu Arg Gln Cys Val Asp Thr
    50                     55                   60
Tyr Trp Ala Glu Asn Gly Ser Leu His Pro Gly Gln Ser Thr Glu Asn
65                     70                     75                   80
Thr Ser Thr Arg Gly Lys Thr Thr Thr Lys Asp Pro Arg Arg Leu Gln
                85                     90                   95
Ala Thr Gly Ala Gly Lys Phe Glu Ser Gly Tyr Val Gln Val Val
        100                    105                   110
```

```
Asp Gly Asp Met His Asp Arg Ser Tyr Ala Val Leu Gly Gly Val Asp
        115                 120                 125
Cys Leu Gly Leu Leu Ala Leu Cys Glu Ser Gly Pro Ile Cys Gln Gly
    130                 135                 140
Asp Thr Trp Ser Glu Asp Gly Asn Phe Cys Arg Cys Thr Phe Ser Glu
145                 150                 155                 160
His Gly Val Ser Cys Cys Lys Lys Pro Lys Ser Lys Ala Thr Thr Ala
                165                 170                 175
Gln Arg Asn Ser Lys Pro Ala Asn Ser Lys Ser Thr Pro Pro Val His
            180                 185                 190
Ser Asp Arg Ala Ser Lys Glu His Asn Pro Ser Gln Gly Glu Gln Pro
        195                 200                 205
Arg Arg Gly Pro Thr Ser Ser Lys Thr Thr Ile Ala Ser Thr Pro Ser
        210                 215                 220
Thr Glu Asp Thr Ala Lys Pro Thr Ile Ser Lys Pro Lys Leu Thr Ile
225                 230                 235                 240
Arg Pro Ser Gln Arg Gly Pro Ser Gly Ser Thr Lys Ala Ala Ser Ser
                245                 250                 255
Thr Pro Ser His Lys Thr Asn Thr Arg Gly Thr Ser Lys Thr Thr Asp
            260                 265                 270
Gln Arg Pro Arg Thr Gly Pro Thr Pro Glu Arg Pro Arg Gln Thr His
        275                 280                 285
Ser Thr Ala Thr Pro Pro Pro Thr Thr Pro Ile His Lys Gly Arg Ala
        290                 295                 300
Pro Thr Pro Lys Pro Thr Thr Asp Leu Lys Val Asn Pro Arg Glu Gly
305                 310                 315                 320
Ser Thr Ser Pro Thr Ala Ile Gln Lys Asn Pro Thr Thr Gln Ser Asn
                325                 330                 335
Leu Val Asp Cys Thr Leu Ser Asp Pro Asp Glu Pro Gln Arg Ile Cys
            340                 345                 350
Tyr Gln Val Gly Thr Tyr Asn Pro Ser Gln Ser Gly Thr Cys Asn Ile
        355                 360                 365
Glu Val Pro Lys Cys Ser Thr Tyr Gly His Ala Cys Met Ala Thr Leu
        370                 375                 380
Tyr Asp Thr Pro Phe Asn Cys Trp Arg Arg Thr Arg Arg Cys Ile Cys
385                 390                 395                 400
Asp Ser Gly Gly Glu Leu Ile Glu Trp Cys Cys Thr Ser Gln
                405                 410
```

```
<210> 18
<211> 13294
<212> DNA
<213> human metapneumo virus

<220>
<221> misc_feature
<222> (0)...(0)
<223> human MPV protein

<400> 18
acgcgaaaaa aacgcgtata aattaaattc caaacaaaac gggacaaata aaaatgtctc   60
ttcaagggat tcacctaagt gatctatcat ataaacatgc tatattaaaa gagtctcaat  120
acacaataaa aagagatgta ggcaccacaa ctgcagtgac accttcatca ttacaacaag  180
aaataacact tttgtgtggg gaaatacttt acactaaaca cactgattac aaatatgctg  240
ctgagatagg aatacaatat atttgcacag ctctaggatc agaaagagta caacagattc  300
tgagaaactc aggtagtgaa gttcaggtgg ttctaaccaa aacatacttc ttagggaaag  360
gcaaaaacag taaaggggaa gagctgcaga tgttagatat acatggagtg gaaaagagtt  420
ggatagaaga aatagacaaa gaggcaagaa agacaatggt aactttgctt aaggaatcat  480
caggtaacat cccacaaaac cagagacctt cagcaccaga cacaccaata attttattat  540
gtgtaggtgc cctaatattc actaaactag catcaacaat agaagttgga ttagagacta  600
cagttagaag agctaataga gtgctaagtg atgcactcaa aagatacccca aggatagata  660
```

17

```
taccaaagat tgctagatct ttttatgaac tatttgaaca aaaagtgtac tacagaagtt 720
tattcattga gtacggaaaa gctttaggct catcttcaac aggaagcaaa gcagaaagtt 780
tgtttgtaaa tatatttatg caagcttatg gagctggcca aacactgcta agagtgggta 840
tcaLtgccag atcatccaac aacataatgc tagggcatgt atctgtgcaa tctgaatcga 900
agcaagttac agaagtttat gacttggtga gagaaatggg tcctgaatct gggctttttac 960
atctaagaca aagtcgaaag gcagggctgt LatcaLtggc caattgcccc aattttgcta 1020
gtgttgttct tggcaatgct tcaggtctag gcataatcgg aatgtacaga gggagagtac 1080
caaacacaga gctattttct gcagcagaaa gttatgccag aagcttaaaa gaaagcaata 1140
aaatcaactt ctcttcgtta gggcttacag atgaagaaaa agaagctgca gaacacttct 1200
taaacatgag tggtgacaat caagatgatt atgagtaatt aaaaaactgg gacaaggtca 1260
aatgtcattc cctgaaggaa aggatattct gttcatgggt aatgaagcag caaaaatagc 1320
cgaagctttc cagaaatcac tgaaaaaatc aggtcacaag agaactcaat ctattgtagg 1380
ggaaaaagtt aacactatat cagaaaatct agaactacct accatcagca aacctgcacg 1440
atcatctaca ctgctggaac caaaattggc atgggcagac aacagcggaa tcaccaaaat 1500
cacagaaaaa ccagcaacca aaacaacaga tcctgttgaa gaagaggaat tcaatgaaaa 1560
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<400> 65
aggcaaatct ctggataatg c                                          21

<210> 66
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 66
tcgtaacgtc tcgtgacc                                              18

<210> 67
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 67
ggagatcttt ctagagtgag                                           20

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> 10, 19
<223> n = A,T,C or G
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<220>
<221> misc_feature
<222> 10, 19
<223> n = A,T,C or G

<400> 68
ccttggtgan tctatccgna g                                         21

<210> 69
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> 17
<223> n = A,T,C or G

<220>
<221> misc_feature
<222> 17
<223> n = A,T,C or G

<400> 69
ctgccactgc tagttgngat aatcc                                     25

<210> 70
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 70
gggcttctaa gcgacccaga tcttg                                     25

<210> 71
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 71
gaatttcctt atggacaagc tctgtgc                                   27

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 72
ggagcaggaa ctccaagacc tggag                                     25
```

```
<210> 73
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 73
gctcaacctc atcacatact aaccc                                    25

<210> 74
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 74
gagatgggcg ggcaagtgcg gcaacag                                  27

<210> 75
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 75
gcctttgcaa tcaggatcca aatttggg                                 28

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 76
ctgctgcagt tcaggaaaca tcag                                     24

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 77
accggatgtg ctcacagaac tg                                       22

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer
```

```
<400> 78
tttgttatag gcatatcatt g                                              21

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 79
ttaaccagca aagtgtta                                                  18

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 80
ttagggcaag agatggtaag g                                              21

<210> 81
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 81
ttataacaat gatggaggg                                                 19

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 82
cattaaaaag ggcacagacg c                                              21

<210> 83
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 83
tggacattct ccgcagt                                                   17

<210> 84
<211> 907
<212> DNA
<213> human metapneumo virus
```

<400> 84
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atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttgg tcctcatagg aataactaca  120
ttgagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagagaaac tccaacggtc  240
cccacagaca acttcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa  300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca  360
ccagatacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc  420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca  480
catttctccac cacgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc  540
agcacaagaa agagaccgtc cacagcatca gtccaacctg acatcagcgc aacaacccac  600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaatacaa  660
aggaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata  720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagccaa aagacaattc  780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa  840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaaactg ggcaaaacaa  900
cacccaa                                                             907
```

<210> 85
<211> 908
<212> DNA
<213> human metapneumo virus

<400> 85
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atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag tgtaaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttgg tcctcatagg aataactaca  120
ttgagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagagaaac tccaacggtc  240
cccacagaca acttcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa  300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca  360
ccagatacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc  420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca  480
catttctccac cacgggcaac gacaaggacg gcacgcagga accaccactc tccgcacaag  540
caaaaacgaa gaagcaagtc cagcgagccc acaaacatct gcaagcacaa caagaataca  600
aaggaaaagc gtggaggcca acacatcaac aacatacaac caaactagtt aacaaaaaat  660
acaaaataac tctaagataa accatgcaga caccaacaat ggagaagcca aaagacaatt  720
cacaatctcc ccaaaaaggc aacaacacca tattagctct gcccaaatct ccctggaaaa  780
aacactcgcc catataccaa aaataccaca accaccccaag aaaaaaaact gggcaaaaca  840
acacccaa                                                           900
                                                                    908
```

<210> 86
<211> 907
<212> DNA
<213> human metapneumo virus

<400> 86
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atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttgg tcctcatagg aataactaca  120
ctgagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagagaaac tccaacggtc  240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa  300
ggctccacac tctactttgc agcctcagca aactcaccag agacagaacc aacatcaaca  360
ccagcacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc  420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccacagaa  480
cactctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc  540
agcacaagaa agagaccgtc cacagcatca gtccaacctg acatcagcgc aacaacacaa  600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacacaa  660
aggaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata  720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc  780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa  840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaaactg ggcaaaacaa  900
```

```
cacccaa                                                            907

<210> 87
<211> 907
<212> DNA
<213> human metapneumo virus

<400> 87
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttgg tcctcatagg aataactaca  120
ttgagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagagaaac tccaacggtc  240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa  300
ggctccacac tctactttgc agcctcagca aactcaccag agacagaacc aacatcaaca  360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc  420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca  480
cattctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc  540
agcacaagaa agagaccgtc cacagcatca gtccaaccg acatcagcgc aacaacccac  600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacaatt  660
aggaaaacgg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata  720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc  780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa  840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaaactg ggcaaaacaa  900
cacccaa                                                            907

<210> 88
<211> 907
<212> DNA
<213> human metapneumo virus

<400> 88
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttgg tcctcatagg aataactaca  120
ttgagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagagaaac tccaacggtc  240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa  300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca  360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc  420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca  480
cattctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc  540
agcacaagaa agagaccgtc cacagcatca gtccaaccg acatcagcgc aacaacccac  600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacaatt  660
aggaaaacgg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata  720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc  780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa  840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaaactg ggcaaaacaa  900
cacccaa                                                            907

<210> 89
<211> 907
<212> DNA
<213> human metapneumo virus

<400> 89
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat   60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca  120
ttgagtatag ccctcaatat ctatctgatc ataaactata caatgcaaga aaacacatct  180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcaggggaaa tccaacggtc  240
cccatagaca atctagacac caactcaagc ccacatcaga caactcaaca gtccacagaa  300
gactccacac tccactctgc agcttcagca agctcaccag agacagaacc aacatcaaca  360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaagc  420
aggacaagga caagtccggc agtccacaca aaaaacaatc caagggtaag ccccagaaca  480
```

45

```
cattccccac catgggcaat gacaaggacg gtccgcggaa ccaccactct ccgcacaagc 540
agcacaagaa aaagactgtc tacagcatca gtccaacccg acagcagcgc aacaacccac 600
aaacacgaag aacaaagccc agtgagccca caaacatctg caagcacagc agaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
caaaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc aaaaaagcaa caacaccata ttagctccgc ttaaatctcc ctgaaaaaa 840
cactcacccca tataccaact ataccacaac catcccaaga aaaaaggctg ggcaaaacaa 900
cacccaa                                                             907
```

`<210> 90`
`<211> 908`
`<212> DNA`
`<213> human metapneumo virus`

`<400> 90`
```
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca 120
ttgagtatag ccctcaatat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ttcatccaccc atggaatcca gcaggggaac tccaacggtc 240
cctattggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gccctttcgtc gacacacaca caacaccatc aagtgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaatc taaggataag ccccagaaca 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcataagaa aaagaccgtc cacagcatca gtccaacctg acagcagcgc aacaacccac 600
aaacacgaag aagcaagccc agtgagcccg caagcatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
taaaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc caaaaaggca acaacaccat attagctccg cttaaatctc ctggaaaaaa 840
cacctcgccc atataccaac tataccacaa ccatcccaag gaaaaagct gggtaaaaca 900
cacccaa                                                             908
```

`<210> 91`
`<211> 908`
`<212> DNA`
`<213> human metapneumo virus`

`<400> 91`
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atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca 120
ttgagtatag ccctcaatat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcatcaccc atggaatcca gcagggaaac tccaacggtc 240
cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gccctttcgtc gacacacaca caacaccatc aagtgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaatc taaggataag ccccagaaca 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcataagaa aaagaccgtc cacagcatca gtccaacctg acagcagcgc aacaacccac 600
aaacacgaag aagcaagccc agtgagcccg caagcatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
tacaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc caaaaaggca acaacaccat attagctccg cttaagtctc ctggaaaaaa 840
cacctcgccc atataccaac tataccacaa ccatcccaag aaaaaaagct gggcaaaaca 900
cacccaa                                                             908
```

`<210> 92`
`<211> 888`
`<212> DNA`
`<213> human metapneumo virus`

`<400> 92`
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atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
```

46

```
cgtgtggcac gtagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagtatag ctctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacaccag ctcaccaccc acagaaccca acaaggaagc ttcaacaatc 240
tccacagaca acccagacat caatccaagc tcacagcatc caactcaaca gtccacagaa 300
aaccccacac tcaaccccgc agcatcagcg agcccatcag aaacagaaac agcatcaaca 360
ccagacacaa caaaccgcct gtcctccgta gacaggtcca cagcacaacc aagtgaaagc 420
agaacaaaga caaaaccgac agtccacaca atcaacaacc caaacacagc ttccagtaca 480
caatccccac cacggacaac aacgaaggca atccgcagag ccaccacttt ccgcatgagc 540
agcacaggaa aagaccaac cacaacatta gtccagtccg acagcagcac cacaacccaa 600
aatcatgagg aaacaggttc agcgaaccca caggcgtctg caagcacaat gcaaaactag 660
cacaccaata atataaaacc aaattagtta acaaaaaatg cgagatagct ctaaagcaaa 720
acatgtaggt accaacaatc aagaaaccaa aagacaactc acaatctccc taaaacagca 780
acgacaccat gtcagctttg ctcaaatctc tctgggagaa acttctaccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaca gcatccaa          888
```

<210> 93
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 93
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atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
cccatagaca acccagacat caatccaaac tcacagcatc caacccaaca gtccacagaa 240
agccccacac tcaaccccgc agcctcggtg agcccatcag aaacagaaac agcatcaaca 300
ccagacacaa caaaaccgcct gtcctccgtg gacagatcca caacagaacc aagtgaaagc 420
caatccccac tacgggcaac aacgaaggca gtcctcagag ccacggcttt ccgcacgagc 480
agcacaggaa aagaccaac cacaacatca gtccagctcg acagcagcac cacaacccaa 540
aatcatgagg aaacaagttc agcgaaccca caggcatctg caagcacaat gcaagaccag 600
cacaccaaca acataaaacc aaattagtta acaaaaaata cgagatagct ctaaagtaaa 720
acatgtaggt accaacaatc aagaaactaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gtcagtttg ctcaaatctc cctgggagaa acttcgccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaca gcacccaa          888
```

<210> 94
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 94
```
atggaggtga aagtagagaa catccgagca gtagacatgc tcaaagcaag agtcaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctccttaa tcctcgtagg aataactaca 120
ctgagcatag ccctcaatat ctatctgatc gtaaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacaccag ctcaccaccc acagaatcca acaaaggaac ttcaacaatc 240
cccacagaca acccagacat caatccaaat tcacaacatc caactcaaca gtccacagaa 300
agccccacac tcaaccccgc agcctcggtg agcccatcag aaacagaaac agcatcaaca 360
ccagacacaa caaaacgcct gtcctccgca gacagatcca caacaaacc aagtgaaagc 420
caatcaccac cacgggcaac aacgaaggcg gtcctcagag acaccgcctt ccacacgagc 480
agcacaggaa aagaccaac cacaacatca gtccagtctg gcagcagcac cacacgagc 540
aatcatgaag aaacaagttc atcgaaccca caggcatctg caagcacaat gcaagaccag 660
cacaccaaca atacaaaaca aaattagtta acaaaaaata caagtagct ctaaagtaaa 720
acatgtaggt accaacagta aagaaatcaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gtcagtttcg ctcaaatctc cctgggagaa actctcgccc acatactaac 840
aacatcacaa ctatctcaag aaaagaaact gggcaaaaa acactcaa          888
```

<210> 95
<211> 887
<212> DNA
```

<213> human metapneumo virus

<400> 95
```
atggaggtga aagtagagaa catccgagca gtagacatgc tcaaagcaag agttaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctcttaa tcctcgtagg aataactaca 120
ctgagtatag ccctcaatat ctatctgatc gtaaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacactag ctcatcaccc acagaatcca acaaaggaac ttcaacaatc 240
ccacagacaa cccagacatc aatcaaatt cacaacatcc aactcaacag tccacagaaca 300
gccccacact caacaccgca gcctcggtga gcccatcaga aacagaacca gcatcaacac 360
cagacacaac aaaccgcctg tcctccgcag acagatccac aacacaacca agtgaaagca 420
gaacaaagac aaagctgaca gtccacacaa aaaacaacct aagtacagcc tccagaacac 480
aatcaccacc acgggcaaca acgaaggcgg tcctcagaga caccgccttc cacacgagca 540
gcacaggaaa aagaccaacc acaacatcag tccagtctgg cagcagcacc acaactcaaa 600
atcatgaaga aacaagttca tcgaacccac aggcatctgc aagcacaatg caagaccagg 660
acaccaacaa tacaaaacaa aattagttaa caaaaaaatac aagatagctc taagtaaaa 720
catgtaggta ccaacagtaa agaaatcaaa agacaactca taatctcccc aaaacagcaa 780
caacatcatg tcagcttcgc tcaaatctcc ctgggagaaa ctctcgccca catactaaca 840
acatcacaac tatctcaaga aaagaaactg ggcaaaaaaa cactcaa   887
```

<210> 96
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 96
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atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag aatgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaagaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcaacccgc agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcct gtcctccgta gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaactgac agtccacaaa aaaacaatcc caagtacagt tctagaaca 480
caatcctcaa tacgggcaac acgaaggcgg gtcctcagaa gtcctcagag gtcctcagac gtgctcaaga gtcctcagac ccacgcctt tcgcacgagc 540
agcacaggag aaagaccaac tacaacatca gtccagtctg acagcagcac cacacccaa 600
aatcatgaag aaacaggttc agcgaaccca caggcatctg caagacaat gcaaaactag 660
cacaccaaca ttgtaaaacc aaattagtta acaaaaaata tgaaatagct ctaaagtaa 720
acatgtaggt gctaacaatc aagaaatcaa aagacaactc ataatctctc caaaacagca 780
acaacatcat gtcaactttg ctcaaatctc cctgggagaa acttctgccc ccatactgac 840
aacatcacaa tcatctcaag aaagaaact gggcaaaaca gcaccaaa   888
```

<210> 97
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 97
```
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaacat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaagaaac ttcaacaatc 240
tctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcagccccac agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
tcagacacaa caagccgcct gtcttccgta gacagatcca caacacaacc aagtgaaagc 420
agagcaagga caaaaccgac agtccacaag aaaaacatcc caagtacagt ttctagaaca 480
caatccccac tacgggcaac aacgaaggcg gtcctcagag ccacgcgctt tcgcacgagc 540
agcacaggag aaggaccaac cacaacatcg gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaaccca caggcatctg caagacaat gcaaaactag 660
cacaccaaca ttgtaaaacc aaattagtta acaaaaaata tgaaatagct ctaaagtaa 720
acatgtaggt gctaacaatc aagaaatcaa aagacaactc ataatctctc caaaacagca 780
acaacatcaa tcatctcaag aaagaaact gggcaaaaca gcaccaaa   840
```

<210> 98
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 98
```
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gtagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagtatag ctctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacaccag ctcaccaccc acagaatcca acaaggaagc ttcaacaatc 240
tccacagaca atccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
aaccccacac taaaccccgc agcatcggtg agctcatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcct gtcctccgta gacaggtcca cagcacaacc aagtgaaagc 420
agaacaagga caaaaccgac agtccacaca agaaaacaacc caagcacagc ttccagcaca 480
caatccccac cacgggtaac aacgaaggca atcctcagag ccaccgtctt ccgcatgagc 540
agcacaggaa aaagaccagc cacaacatta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcaaactca caggcatctg caagcacaat gcaaaactag 660
cactccaaca atataaaacc aaattagtta acaaaaaata cgagtagct ctaaagtaaa 720
acatgtaggc accaacaatc aggaaattaa aagacaactc acaactctcc taaaacagca 780
acgacaccat gtcaactttg ctcaaatctc tctgggagaa acttttgccc acatactaac 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaca gcatccaa   888
```

<210> 99
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 99
```
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaacat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatca acaaagaaac ttcaacaatc 240
tctatagaca actcagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcagcccac agcctcggtg agcctcatcag aaacagaacc agcatcaaca 360
tcagacacaa caaaccgcct gtcttccgta gacagatcca caacacaacc aagtgaaagc 420
agagcaagaa caaaaccgac agtccacaag aaaaacatcc caagtacagt ttctagaaca 480
caatccccac tacgggcaac aacgaaggcg gtcctcagag ccaccgcctt tcgcatgagc 540
agcacaggaa agggaccaac cacaacatcg gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca ttgcaaaacc aaattagtta acaaaaaata tgaaatagtt ctaaagtaaa 720
acatgtaggt gccaacaatc aagaaattca aagacaactc acaatctccc taaaacagca 780
acaacatcat gccaactttg ctcaaatctc cctgggagaa accctcgccc ccatactgac 840
aacatcacaa tcatctcaag · aaaagaaact gggcaaaaca gcaccaaa   888
```

<210> 100
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 100
```
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatca acaaggaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tctacccac atcctcggtg agctcatcag aaacagaacc agcatcaaca 360
ccaggcataa caaaccacct gtctttcgta gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaccggac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
cagtccccac cacggacaac agcgaaggcg gtccccagag ccaccgccct tcgcacgacc 540
agcacaggag aaagaccaac cacgaacccg atagcagcac cacaacacaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca ttgcaagacc aaattagtta acaaaaaata tgaaatagct ctaaagtaaa 720
```

49

```
acatgtaggt gccaacaatc aagaaaatcaa aagataactc ataatctctc taaaacatca 780
acaacatcat gttaactttg ctcaaatctc tctgggagaa accttcgccc ccatactggc 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaca acaccaaa            888
```

```
<210> 101
<211> 888
<212> DNA
<213> human metapneumo virus
```

```
<400> 101
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccgcagaa 300
agcctcacac tctacccccac atcctcggtg agctcatcag aaacagaacc agcatcaaca 360
ccaggcataa caaaccacct gtcctttgta gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaccggac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
cagtccccac cacggacaac agcgaaggcg gtccccagag ccaccgccct tcgcacgagc 540
agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
aatcatgaag aaacaggctc agcgaacccca caggcatccg caagcaacat gcaaaaccaa 660
cacaccaaca ttgcaagacc aaattagtta acaaaaaata tgaaatagct ctaaagtaaa 720
acatgtaggt gccaacaatc aagaaatcaa aagataactc ataatctctc taaaacatca 780
acaacatcat gttaactttg ctcaaatctc tctgggagaa accttcgccc ccatactggc 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaca acaccaaa            888
```

```
<210> 102
<211> 888
<212> DNA
<213> human metapneumo virus
```

```
<400> 102
atggaggtga aagtagagaa tattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccgcagaa 300
agcctcacac tctacccccac atcctcggtg agctcatcag aaacagaacc agcatcaaca 360
ccaggcataa caaaccacct gtcctttgta gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaccggac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
cagtccccac cacggacaac agcgaaggcg gtccccagag ccaccgccct tcgcacgagc 540
agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
aatcatgaag aaacaggctc agcgaacccca caggcatccg caagcacaat gcaaaaccaa 660
cacaccaaca ttgcaagacc aaattagtta acaaaaaata tgaaatagct ctaaagtaaa 720
acatgtaggt gccaacaatc aagaaatcaa aagataactc ataatctctc taaaacatca 780
acaacatcat gttaactttg ctcaaatctc tctgggagaa accttcgccc ccatactggc 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaca acacccaa            888
```

```
<210> 103
<211> 888
<212> DNA
<213> human metapneumo virus
```

```
<400> 103
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gtagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagcatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaggaaac ttcaacaatc 240
tccacagaca acccagacat caatccaaac tcacagcatc caactcaaca gtcccacagaa 300
aaccccacac tcaacccagc agcatcaggcg agcccatcag aaacagaatc agcatcaaca 360
ccagatacaa caaaccgcct gtcctccgta gacaggtcca cggtacaacc aagtgaaaac 420
agaacaaaga caaaactgac agtccacaca agaaacaacc taagcacagc ctccagtaca 480
```

```
caatccccac cacgggcaac aacgaaggca atccgcagag ccaccaccct ccgcatgagc 540
agcacaggaa gaagaccaac cacaacacta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca atataaaacc aaattagtta acaaaaaata cgagatagct ctaaagtaaa 720
acatgtaggc accaacaatc aagaaaccaa aagataactc acaatccccc caaaacagca 780
acgacaccat gtcagctttg ctcaaatctc tctgggagaa acttttgccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaca gcatccaa              888
```

<210> 104
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 104
```
atggaggtga aagtagagaa cattccgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gtagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagcatag ccctcaatat ctatctgatc ataaatacta caatacaaaa aaccacatct 180
gaatcagaac accacaccag ctcaccaccc acagaatcca acaaggaagc ttcaacaatc 240
tccacagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
aaccccacac tcaaacccagc agcatcagcg agcccatcag aaacagaatc agcatcaaca 360
ccagatacaa caaaccgcct gtcctccgta gacaggtcca cggtacaacc aagtgaaaac 420
agaacaaaga caaaactgac agtccacaca agaaacaacc taagcacagc ctccagtaca 480
caatccccac cacgggcaac aacgaaggca atccgcagag ccaccaccct ccgcatgagc 540
agcacaggaa gaagaccaac cacaacacta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca atataaaacc aaattagtta acaaaaaata cgagatagct ctaaagtaaa 720
acatgtaggc accaacaatc aagaaaccaa aagataactc acaatccccc caaaacagca 780
acgacaccat gtcagctttg ctcaaatctc tctgggagaa acttttgccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaca gcatccaa              888
```

<210> 105
<211> 901
<212> DNA
<213> human metapneumo virus

<400> 105
```
atggaagtaa gagtggagaa cattccgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg aactaacgcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa actgtgctaa catgccgtcg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacagag 300
aactcaacat ccccagtagc aacccagagg ggccatccat acacagggac aactcaacaa 360
tcagacacaa cagctcccca gcaaaccaca gacaaacaca cagcaccgct aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa tcagagcaac aaccccaaaa 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaggca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcaa aaatgcaagt gagacaatca caacatccga cagacccaga 600
actgacacca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
ccacaccatg catagagagg tgcaaaactc aaatgagcac aacacacaaa catcccatcc 720
aagtagttaa caaaaaacca caaaataacc ttgaaaacca aaaaaccaaa acataaaccc 780
agacccagaa aaacatagac accatatgga aggttctagc atatgcacca atgagatggc 840
atctgttcat gtatcaatag caccaccatc attcaaggaa taagaagagg cgaaaattta 900
a                                                                 901
```

<210> 106
<211> 901
<212> DNA
<213> human metapneumo virus

<400> 106
```
atggaagtaa gagtggagaa cattccgagcg atagacatgt tcaaagcaaa gataaagaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc attgatcatg caacattaag aaacatgatc 180
```

```
aaaacagaaa actgtgctaa catgccatcg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaagcac cgaaccccat ccacagcaag caacacaatg gaccacagag 300
aactcaacat ccccagcagc aaccctagag agccatccat acacagggac aacccaaaca 360
ccagacataa cagctcccca acaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgacagaa tcaccccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaaa 480
agggaaaaag aaaaagaaaa cacaaaccaa accacaagca gcgtcccca ccaacaacc 540
aacaccacca accaaaccag aaatgcaagt gagacaatca caacatccga cagacccaga 600
attgacacca caacccaaag cagcgatcag acaacccggg caacagaccc aagctcccca 660
ccacaccatg cacagagtgg tgcaaaaccc aaatgaacac aacacacaaa catctcatcc 720
aagtagttaa caaaaaacca caaaataacc ttgaaaacca aaaaaccaaa ccacaaactt 780
agacccagaa aaacatagac actatatgga aggtttgagc atatgcacca atgaaatggt 840
atctgttcat gtatcaatag cgccaccatt atttaaggaa taagaagagg caaaaattca 900
a                                                                901
```

```
<210> 107
<211> 860
<212> DNA
<213> human metapneumo virus
```

```
<400> 107
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatt caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccgccg gcagaaccaa gcaaaaagac cccaatgacc 240
tctacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacgggag 300
aactcaacat tcccagcagc aacctcagag ggccatctac acacagggac aacctcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaaa tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag ggaaagaaaa cacaaaccaa accacaagca gcgtcgctac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagacccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
ccacatcatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gacccagaaa aacatagaca ctatatggaa ggtccgagcx 780
tatgcaccga tgaaatggca tttgttcatg tatcaatagc gccaccatta tttaaggaat 840
aagaagaggc aaaaattcaa                                            860
```

```
<210> 108
<211> 861
<212> DNA
<213> human metapneumo virus
```

```
<400> 108
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccgccg gcagaaccaa gcagaaagac cccaatgacc 240
tccacagcgg gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacgggag 300
aactcaacat ccccagcagc aaccccagag ggccatctac acacagggac aacctcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagaaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaagca gcgtcgcaac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagacccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
gcacaccatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatc acagaaccag aaaaacagac actatatgga aggtccgagc 780
atatgcaccg atgaaatggc atctgttcat gtatcaatag caccaccatt atttaaggaa 840
taagaagagg caaaaattca a                                          861
```

```
<210> 109
<211> 860
<212> DNA
<213> human metapneumo virus
```

```
<400> 109
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac  60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccaccg gcagaaccaa gcaaaagac cccaatgacc 240
tccacagcag gcctaaacac taaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat ccccagcagc aaccccagag ggccatctac acacagggac aactcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaagcaca cagcactgcc aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagacccaga 600
actgactcca caacccaaag cagcgaacag caacacccgg caacagaccc aagctcccca 660
ccacaccatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gacccagaaa acatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcatg tatcaatagc gccaccatta tttaaggaat 840
aagaagaggc aaaaattcaa                                             860
```

```
<210> 110
<211> 860
<212> DNA
<213> human metapneumo virus
```

```
<400> 110
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac  60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccgccg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat ccccagcagc aaccccagag ggccatctac acacagggac aactcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaatt gagacaatca caacatccga cagacccaga 600
actgactcca caacccaaag cagcgaacag caacacccgg caacagaccc aagctcccac 660
ccacaccatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gacccagaaa acatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcatg tatcaatagc gccaccatta tttaaggaat 840
aagaagaggc aagaattcaa                                             860
```

```
<210> 111
<211> 886
<212> DNA
<213> human metapneumo virus
```

```
<400> 111
atggaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa aatgaaaaac  60
cgtataagaa gtagcaggtg ctatagaaat gctacactga tccttattgg attaacagca 120
ttaagtatgg cacttaatat tttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt ggccgcagag 300
gattcaacat ctctagcagc aacctcagag ggccatctac acacagggac aactcaaaca 360
aacagcagga ccacccaaac aaccacagag aaaaagccaa ccggagcaac aaccaaaaa 480
gaaaccacaa ctcgaactac aagcacagct ccaacccaaa cactcaacac taccaaccaa 540
actagctatg tgagagaggc aaccacaaca tccgccagt ccagaaacag tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaaccaca ccatacacag 660
aacaacatca caacaacata caacacagac acatcctctc caagtagtta acaaaaaac 720
tataaaataa tcatgaaac cgaaaaacta gaaaagttaa tttgaactca gaaagaaca 780
caaacctat atgaattgtt tgagcgtata tactaatgaa atagcatctg tttgtgcatc 840
aataataccg tcattatttta agaaataaga agaagctaaa attcaa                886
```

```
<210> 112
```

<211> 889
<212> DNA
<213> human metapneumo virus

<400> 112
atggaagtaa gagtggagaa cattcggaca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gcagcaagtg ctatagaaat gctacactga tccttattgg actgacagca 120
ttaagtatgg cacttaatat tttcttgatc atcgattatg caacatttaa aaacatgacc 180
aaagtggaac actgtgctaa tatgccgccg gtagaaccga gtaagaagac cccaatgacc 240
tctacagtag actcaagcac cggacccaat ccacagcaga caacacagtg gaccacagag 300
gattcaacat ctctagcagc aacctcagag gaccatctac acacagggac aactccaaca 360
ctagatgcaa cagtttctca gcaaacccca gacaagcaca caacaccgct gagatcaacc 420
aatggacaga ccacccagac aaccacagag aaaaagccaa ccagagcaat agccaaaaaa 480
gaaaccacaa accaaaccac aagcacagct gcaacccaaa cattcaacac caccaatcaa 540
accagaaatg gaagagagac aaccataaca tctgccagat ccagaaacga cgccacaact 600
caaagcagcg aacaaacaaa ccagcaaaca gacccaagct cccaaccaca tcatgcatag 660
ataagcacaa taacaatatg aaccacaacac agacacatct tctccaagta gttaacaaaa 720
aactataaaa taaccatgaa aactsaaaaa ctagaaaagt aaatttgaac tcagaaaaga 780
acacaaacac taaatgaatt gtttgagcat atatactaat gaaatagcat ctgttcatgc 840
atcaataata ccatcattac ttaagaaata agaagaagca aaaattcaa   889

<210> 113
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 113
atggaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ttaagtatgg cacttaatat tttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaactcaat ccacagcagg caacacagtt gaccacagag 300
gattcaacat ctctagcagc aacctcggag gatcatttac tcacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa cCggagcaac aaccacaaaa 480
gaaaccacaa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
actagcaatg gaagagaggc aaccacaaca tccaccagat ccagaaacgt tgccacaact 600
caaaacagcg atcaaacaac ctagacagca gacccaagct cccaaccaca ccatacacag 660
aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta acaaaaaact 720
ataaataac catgaaaact aaaaaactag aaaagttaat ttgaactcag aaaagaacac 780
aaacactata tgaattgttt gagcgtatat actaatgaaa tagcatctgt ttgtgcatca 840
ataataccat cattatttaa gaaataagaa gaagctaaaa ttcaa   885

<210> 114
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 114
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgcataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ttaagtatgg cacttaatat tttttaatc attgattatg caacattaaa aaacatgacc 180
aaagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaatcaat ccacagcagg caacacagtt gaccacagag 300
gattcaacat ctctagcagc aacctcagag ggccatcac acacaggaac aactccaaca 360
ccagacgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac agccacagag aaaaagccaa ctggagcaac aaccaaaaaa 480
gaaaccacaa ccgaactac aagtacagct gcaacccaaa cacccaacac caccaaccaa 540
accagcaatg gaagagaggc aaccacaaca tccgccaggt ccagaaacgt tgccacaact 600
caaaacagcg atcaaacaac ccaggcagca gactcaagct cccaaccaca ccatacacag 660
aaaagcacaa caacagcata caacacagac acatcttttc caagtagtta acaaaaaact 720
ataaaataac catgaaaacc aaaaaactag aaaagttaat ttgaactcag aaaagaacac 780

```
aaacactata tgaattgttt gagcgtatat actaatgaaa tagcatctgt ttgtgcatca 840
ataataccat cattatttaa gaaataagaa gaagctaaaa ttcaa              885

<210> 115
<211> 886
<212> DNA
<213> human metapneumo virus

<400> 115
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ctaagtatgg cacttaatat tttttaatc attgattatg caacattaaa aaacatgacc 180
aaagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag actcaaacac caaacccaat ccacagcagg caacacagtt gaccacagag 300
gattctacat ctttagcagc aaccctagag gaccatccac acacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac aactgcagag aaaaagccaa ccagggcaac aaccaaaaaa 480
gaaaccacaa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
actagcaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg atcaaacac ccagtcagca gaaccaagct cccatcaca acatacacag 660
aaaagcacaa caacaacata caacacagac acatcttctc taagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaacta gaaaagttaa tttgaactca gaaaagaaca 780
caaacactat atgaattatt tgagcgtata tactaatgaa atagcatctg tttgtgcatc 840
aataataccat tcattatttta agaaataaga agaagctaaa attcaa             886

<210> 116
<211> 887
<212> DNA
<213> human metapneumo virus

<400> 116
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attatcagca 120
ctaagtatga cacttaatat tttttttaatc attgattatg caaaatcaaa aaacatgacc 180
agagtggaac actgtgttca tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcggg caacacagtt gaccacagag 300
gattcaacat ctctcagcagc aaccctagag ggccatctac acacagggac aactccaaca 360
ccagatgtaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac agccgcagag aaaaagccaa ccagagtaac aactaacaaa 480
gaaaccataa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
accaacaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaatcaca acatacacag 660
aaaagcataa caacaacata caacacagac acatcttctc caagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaaact agaaaagtta atttgaactc agaaaagaac 780
acaaacacta tatgaattgt ttgagcgtat atactaatga aatagcatct gtttgtgcat 840
caataataccc atcattttt aagaattaag aagaagctaa aattcaa            887

<210> 117
<211> 887
<212> DNA
<213> human metapneumo virus

<400> 117
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attatcagca 120
ctaagtatgg cacttaatat tttttaatc attgattatg caaaatcaaa aaccatgacc 180
agagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt gaccacagag 300
gattcaacat ctccagtagc aacctagag ggccatctac acacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaacccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac aaccgcagag aaaagccaa ccagagcaac aaccaaaaaa 480
gaaaccataa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
```

```
accagcaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaatcaca acatacaaag 660
aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaaact agaaaagtta atttgaactc agaaaagaac 780
acaaacacta tatgaattgt ttgagcgtat atactaatga aatagcatct gtttgtgcat 840
caataatacc atcattattt aagaattaag aagaagctaa aattcaa          887
```

<210> 118
<211> 886
<212> DNA
<213> human metapneumo virus

<400> 118
```
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ctaagtatgg cacttaatat tttttaatc attgattatg caacattaaa aacatgacc 180
aaagtggaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt gaccacagag 300
gacttacaat cttttagcagc aaccctaggag gaccatccac acacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccaccaaaca aaaaagccaa ccagagcaac aaccaaaaaa 480
gaaaccacaa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
actagcaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg atcaaacaac ccaggcagca gaaccaaact cccaatcaca acatacacag 660
aaaagcacaa caacaacata caacacagac acatcttctc taagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaacta gaaagttaa tttgaactca gaaaggaaca 780
caaacactat atgaattatt tgagcgtata tactaatgaa atagcatctg tttgtgcatc 840
aataatacca tcattattta agaaataaga agaagctaaa attcaa         886
```

<210> 119
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 119
```
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                  70                  75                  80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
            100                 105                 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
        115                 120                 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
    130                 135                 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145                 150                 155                 160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
                165                 170                 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180                 185                 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
        195                 200                 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
```

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```
     210                215                220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                230                235


<210> 120
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 120
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
 1               5                10                15
Ser Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
           20                25                30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
       35                40                45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
     50                55                60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                70                75                80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
               85                90                95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
           100                105                110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
       115                120                125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
     130                135                140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145                150                155                160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
               165                170                175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
           180                185                190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
       195                200                205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
     210                215                220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                230                235


<210> 121
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 121
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
 1               5                10                15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
           20                25                30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
       35                40                45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
     50                55                60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                70                75                80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
               85                90                95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Asn Ser
```

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```
                100                      105                      110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
            115                      120                      125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
        130                      135                      140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145                      150                      155                  160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
                    165                      170                      175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Ala Gln
                180                      185                      190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
            195                      200                      205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
        210                      215                      220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                      230                      235


<210> 122
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 122
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1                       5                       10                      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                      25                      30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
            35                      40                      45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
        50                      55                      60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                      70                      75                      80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
                85                      90                      95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Asn Ser
            100                     105                     110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asp Arg Pro Pro
        115                     120                     125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130                     135                     140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145                     150                     155                 160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
                165                     170                     175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180                     185                     190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
        195                     200                     205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
    210                     215                     220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                     230                     235


<210> 123
<211> 236
<212> PRT
<213> human metapneumo virus
```

```
<400> 123
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                  70                  75                  80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
            100                 105                 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asp Arg Pro Pro
        115                 120                 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
    130                 135                 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145                 150                 155                 160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
                165                 170                 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180                 185                 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
        195                 200                 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
    210                 215                 220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                 230                 235


<210> 124
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 124
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                  70                  75                  80
Pro Ile Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Asp Ser Thr Leu His Ser Ala Ala Ser Ala Ser Ser
            100                 105                 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
        115                 120                 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Arg Thr
    130                 135                 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Val Ser Pro Arg Thr
145                 150                 155                 160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
                165                 170                 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Leu Ser Thr Ala Ser Val Gln
```

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```
                    180                   185                  190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Thr Ser Pro Val
        195                   200                  205
Ser Pro Gln Thr Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
    210                   215                  220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                   230                  235


<210> 125
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 125
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1                   5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
        20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65                  70                  75                  80
Pro Met Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Gly Ser Thr Leu His Phe Ala Ala Ser Ala Ser Ser
            100                 105                 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
        115                 120                 125
Phe Val Asp Thr His Thr Thr Pro Ser Ser Ala Ser Arg Thr Lys Thr
    130                 135                 140
Ser Pro Ala Val His Thr Lys Asn Asn Leu Arg Ile Ser Pro Arg Thr
145                 150                 155                 160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
                165                 170                 175
Leu Arg Thr Ser Ser Ile Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180                 185                 190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Ala Ser Pro Val
        195                 200                 205
Ser Pro Gln Ala Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
    210                 215                 220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                 230                 235


<210> 126
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 126
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1                   5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
        20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
```

```
65                      70                  75                  80
Pro Met Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
                    85                  90                  95
Gln Ser Thr Glu Gly Ser Thr Leu His Phe Ala Ala Ser Ala Ser Ser
                100                 105                 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
            115                 120                 125
Phe Val Asp Thr His Thr Thr Pro Ser Ser Ala Ser Arg Ile Arg Thr
        130                 135                 140
Ser Pro Ala Val His Thr Lys Asn Asn Leu Arg Ile Ser Pro Arg Thr
    145                 150                 155                 160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
                165                 170                 175
Leu Arg Thr Ser Ser Ile Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180                 185                 190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Ala Ser Pro Val
        195                 200                 205
Ser Pro Gln Ala Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
    210                 215                 220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225                 230                 235
```

<210> 127
<211> 228
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 127
```
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1                   5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
                20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
            35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
        50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Pro Asn Lys Glu Ala Ser Thr Ile
65                  70                  75                  80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Ser Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Lys Pro Thr Val His Thr Ile Asn Asn Pro Asn Thr Ala Ser Ser Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Thr Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
                165                 170                 175
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Leu Val Gln
            180                 185                 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Asn
    210                 215                 220
```

```
Ile Lys Pro Asn
225


<210> 128
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 128
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Lys Pro Thr Val His Thr Lys Asn Asn Pro Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
                165                 170                 175
Phe Arg Thr Ser Ser Thr Arg Lys Arg Pro Thr Thr Thr Ser Val Gln
            180                 185                 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Ser Gln His Thr Asn Asn
    210                 215                 220
Ile Lys Pro Asn
225


<210> 129
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 129
Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
65                  70                  75                  80
Pro Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
            100                 105                 110
```

```
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
                165                 170                 175
Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Ser Val Gln
                180                 185                 190
Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
            195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
    210                 215                 220
Thr Lys Gln Asn
225
```

<210> 130
<211> 228
<212> PRT
<213> human metapneumo virus

<220>
<221> VARIANT
<222> 81
<223> Xaa = Any Amino Acid

<400> 130
```
Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
                20                  25                  30
Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Leu Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
65                  70                  75                  80
Xaa Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
                100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
                165                 170                 175
Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Ser Val Gln
                180                 185                 190
Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
            195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
    210                 215                 220
Thr Lys Gln Asn
225
```

<210> 131

```
<211> 228
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 131
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Met Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Ser Leu Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Lys Leu Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Ser Ile Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
                165                 170                 175
Phe Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Ser Val Gln
            180                 185                 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile
    210                 215                 220
Val Lys Pro Asn
225


<210> 132
<211> 228
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 132
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
```

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```
65                      70                      75                      80
Ser Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                    85                      90                      95
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro
                100                     105                     110
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Ser Arg Leu Ser
            115                     120                     125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr
        130                     135                     140
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
    145                     150                     155                     160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
                    165                     170                     175
Phe Arg Thr Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln
                180                     185                     190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
            195                     200                     205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile
        210                     215                     220
Val Lys Pro Asn
225


<210> 133
<211> 228
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 133
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1                   5                       10                      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
                20                      25                      30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                      40                      45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                      55                      60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65                      70                      75                      80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                    85                      90                      95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Ser
                100                     105                     110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
            115                     120                     125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
        130                     135                     140
Lys Pro Thr Val His Thr Arg Asn Asn Pro Ser Thr Ala Ser Ser Thr
    145                     150                     155                     160
Gln Ser Pro Pro Arg Val Thr Thr Lys Ala Ile Leu Leu Arg Ala Thr Val
                165                     170                     175
Phe Arg Met Ser Ser Thr Thr Gly Lys Arg Pro Ala Thr Thr Leu Val Gln
                180                     185                     190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
            195                     200                     205
Asn Ser Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Ser Asn Asn
        210                     215                     220
```

```
Ile Lys Pro Asn
225
```

```
<210> 134
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 134
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
        50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Ser Ile Asp Asn Ser Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
            85                  90                  95
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Asn Arg Leu Ser
        115                 120                 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr
        130                 135                 140
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
            165                 170                 175
Phe Arg Met Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln
        180                 185                 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
    210                 215                 220
Ala Lys Pro Asn
225
```

```
<210> 135
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 135
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
        50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
            85                  90                  95
Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
            100                 105                 110
```

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```
Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
        115                 120                 125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
                165                 170                 175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
                180                 185                 190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
    210                 215                 220
Ala Arg Pro Asn
225


<210> 136
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 136
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1               5                  10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
                20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Ala Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
        115                 120                 125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                 135                 140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
                165                 170                 175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
                180                 185                 190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
        195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
    210                 215                 220
Ala Arg Pro Asn
225


<210> 137
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 137
```

```
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1               5                  10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65                  70                  75                  80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
            100                 105                 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
            115                 120                 125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
        130                 135                 140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
                165                 170                 175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
            180                 185                 190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
            195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
    210                 215                 220
Ala Arg Pro Asn
225
```

```
<210> 138
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 138
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1               5                  10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Gln Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65                  70                  75                  80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
            100                 105                 110
Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
            115                 120                 125
Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
        130                 135                 140
Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
                165                 170                 175
Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
            180                 185                 190
```

```
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
    195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
    210                 215                 220
Ile Lys Pro Asn
225


<210> 139
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 139
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1               5                   10                  15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
        20                  25                  30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35                  40                  45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50                  55                  60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65                  70                  75                  80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
                85                  90                  95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
            100                 105                 110
Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
    115                 120                 125
Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
    130                 135                 140
Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
145                 150                 155                 160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
                165                 170                 175
Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
                180                 185                 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
    195                 200                 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
    210                 215                 220
Ile Lys Pro Asn
225


<210> 140
<211> 231
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 225
<223> Xaa = unknown amino acid or other

<400> 140
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
        20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
```

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```
        35                    40                    45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                    55                    60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                    70                    75                    80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                  85                    90                    95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro Glu Gly His
                  100                   105                   110
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala Pro Gln Gln
        115                   120                   125
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn Glu Gln Ile
    130                   135                   140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr Gln Lys
145                   150                   155                   160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
                  165                   170                   175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
        195                   200                   205
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Thr Gln Ser Ser
    210                   215                   220
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
Xaa Arg Gly Ala Lys Leu Lys
225                   230
```

<210> 141
<211> 231
<212> PRT
<213> human metapneumo virus

<400> 141

```
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
 1               5                    10                   15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
            20                   25                   30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                   40                   45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                   55                   60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                   70                   75                   80
Ser Thr Ala Gly Pro Ser Thr Glu Pro Asn Pro Gln Gln Ala Thr Gln
                  85                   90                   95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Leu Glu Ser His
                  100                  105                  110
Pro Tyr Thr Gly Thr Thr Gln Thr Pro Asp Ile Thr Ala Pro Gln Gln
        115                  120                  125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
    130                  135                  140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Lys
145                  150                  155                  160
Arg Glu Lys Glu Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
                  165                  170                  175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Thr Arg Asn Ala Ser Glu Thr
        195                  200                  205
Ile Thr Thr Ser Asp Arg Pro Arg Ile Asp Thr Thr Thr Gln Ser Ser
Asp Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
    210                  215                  220
Gln Ser Gly Ala Lys Pro Lys
```

70

```
        225                        230
```

<210> 142
<211> 231
<212> PRT
<213> human metapneumo virus

<400> 142
```
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                  55                  60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                  90                  95
Trp Thr Thr Glu Asn Ser Thr Phe Pro Ala Ala Thr Ser Glu Gly His
            100                 105                 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
        115                 120                 125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
    130                 135                 140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145                 150                 155                 160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
                165                 170                 175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
            180                 185                 190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
        195                 200                 205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
    210                 215                 220
Gln Gly Ser Ala Lys Pro Lys
225                 230
```

<210> 143
<211> 231
<212> PRT
<213> human metapneumo virus

<400> 143
```
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                  55                  60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Arg Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                  90                  95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
            100                 105                 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
```

```
        115                    120                    125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
    130                    135                    140
Thr Gln Ala Thr Thr Glu Lys Lys Thr Thr Arg Glu Thr Thr Gln Arg
145                    150                    155                    160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
                165                    170                    175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
            180                    185                    190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
        195                    200                    205
Glu Gln Thr Thr Gln Ala Thr Asp Pro Ser Ser Pro Ala His His Ala
    210                    215                    220
Gln Gly Ser Ala Lys Pro Lys
225                    230
```

```
<210> 144
<211> 231
<212> PRT
<213> human metapneumo virus
```

```
<400> 144
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1                    5                     10                    15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
            20                    25                    30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                    40                    45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                    55                    60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                    70                    75                    80
Ser Thr Ala Gly Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                    90                    95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
            100                   105                   110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
        115                   120                   125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
    130                   135                   140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145                   150                   155                   160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
                165                   170                   175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
            180                   185                   190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
        195                   200                   205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
    210                   215                   220
Gln Gly Ser Ala Lys Pro Lys
225                   230
```

```
<210> 145
<211> 231
<212> PRT
<213> human metapneumo virus
```

```
<400> 145
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
```

```
1                    5                    10                   15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
                20                   25                   30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
          35                   40                   45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
     50                   55                   60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                   70                   75                   80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
               85                   90                   95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
             100                  105                  110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
          115                  120                  125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
       130                  135                  140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145                  150                  155                  160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
               165                  170                  175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Ala Asn Ala Ile Glu Thr
             180                  185                  190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
          195                  200                  205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser His Pro His His Ala
     210                  215                  220
Gln Gly Ser Ala Lys Pro Lys
225                  230
```

```
<210> 146
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 146
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1                    5                    10                   15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
                20                   25                   30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
          35                   40                   45
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His
     50                   55                   60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                   70                   75                   80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
               85                   90                   95
Leu Ala Ala Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
             100                  105                  110
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
          115                  120                  125
Thr Thr Asp Glu Tyr Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
       130                  135                  140
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145                  150                  155                  160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
               165                  170                  175
Thr Thr Asn Gln Thr Ser Tyr Val Arg Glu Ala Thr Thr Thr Ser Ala
             180                  185                  190
Arg Ser Arg Asn Ser Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
```

73

```
          195                    200                    205
Ala Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
    210                    215                    220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225                    230                    235
```

```
<210> 147
<211> 236
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 220, 227
<223> Xaa = unknown amino acid or other

<400> 147
Met Glu Val Arg Val Glu Asn Ile Arg Thr Ile Asp Met Phe Lys Ala
1               5                  10                  15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp Tyr Ala Thr Phe Lys Asn Met Thr Lys Val Glu His
    50                  55                  60
Cys Ala Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Thr Val Asp Ser Ser Thr Gly Pro Asn Pro Gln Gln Thr Thr Gln
            85                  90                  95
Trp Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
        100                 105                 110
Leu His Thr Gly Thr Thr Pro Thr Leu Asp Ala Thr Val Ser Gln Gln
    115                 120                 125
Thr Pro Asp Lys His Thr Thr Pro Leu Arg Ser Thr Asn Gly Gln Thr
130                 135                 140
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Arg Ala Ile Ala Lys Lys
145                 150                 155                 160
Glu Thr Thr Asn Gln Thr Thr Ser Thr Ala Ala Thr Gln Thr Phe Asn
            165                 170                 175
Thr Thr Asn Gln Thr Arg Asn Gly Arg Glu Thr Thr Ile Thr Ser Ala
        180                 185                 190
Arg Ser Arg Asn Asp Ala Thr Thr Gln Ser Ser Glu Gln Thr Asn Gln
    195                 200                 205
Thr Thr Asp Pro Ser Ser Gln Pro His His Ala Xaa Ile Ser Thr Ile
    210                 215                 220
Thr Ile Xaa Thr Gln His Arg His Ile Phe Ser Lys
225                 230                 235
```

```
<210> 148
<211> 236
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 208
<223> Xaa = unknown amino acid or other

<400> 148
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
```

74

```
     1                    5                    10                   15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
                 20                   25                   30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
         35                   40                   45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
     50                   55                   60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                   70                   75                   80
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln
                 85                   90                   95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
             100                  105                  110
Leu Leu Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
         115                  120                  125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
     130                  135                  140
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145                  150                  155                  160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
             165                  170                  175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Thr
         180                  185                  190
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Thr Thr Xaa
     195                  200                  205
Thr Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
     210                  215                  220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225                  230                  235
```

```
<210> 149
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 149
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
 1                    5                    10                   15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
                 20                   25                   30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
         35                   40                   45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
     50                   55                   60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                   70                   75                   80
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln
                 85                   90                   95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Gly His
             100                  105                  110
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
         115                  120                  125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
     130                  135                  140
Thr Gln Thr Ala Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145                  150                  155                  160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Pro Asn
             165                  170                  175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Gln Ala Thr Thr Thr Ser Ala
         180                  185                  190
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Ile Thr Gln
     195                  200                  205
```

```
Ala Ala Asp Ser Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
    210                 215                 220
Thr Ala Tyr Asn Thr Asp Thr Ser Phe Pro Ser Ser
225                 230                 235
```

```
<210> 150
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 150
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
    50                  55                  60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Ala Val Asp Ser Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                  90                  95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Asp His
                100                 105                 110
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
            115                 120                 125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
    130                 135                 140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
145                 150                 155                 160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
                165                 170                 175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
            180                 185                 190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
        195                 200                 205
Ala Ala Glu Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr
    210                 215                 220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Leu Ser Ser
225                 230                 235
```

```
<210> 151
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 151
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Ser Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp Tyr Ala Lys Ser Lys Asn Met Thr Arg Val Glu His
    50                  55                  60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Arg Ala Thr Gln
                85                  90                  95
```

```
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Gly His
            100                     105                 110
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Val Thr Val Ser Gln Gln
        115                     120                 125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
    130                     135                 140
Thr Gln Thr Ala Ala Glu Lys Lys Pro Thr Arg Val Thr Thr Asn Lys
145                     150                 155                 160
Glu Thr Ile Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
                165                 170                 175
Thr Thr Asn Gln Thr Asn Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
            180                 185                 190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
        195                 200                 205
Ala Ala Asp Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Ile Thr
    210                 215                 220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225                 230                 235
```

```
<210> 152
<211> 236
<212> PRT
<213> human metapneumo virus
```

```
<400> 152
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Ser Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp Tyr Ala Lys Ser Lys Thr Met Thr Arg Val Glu His
    50                  55                  60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                  90                  95
Leu Thr Thr Glu Asp Ser Thr Ser Pro Ala Ala Thr Leu Glu Gly His
            100                     105                 110
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
        115                     120                 125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
    130                     135                 140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
145                     150                 155                 160
Glu Thr Ile Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
                165                 170                 175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
            180                 185                 190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
        195                 200                 205
Ala Ala Asp Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr
    210                 215                 220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225                 230                 235
```

```
<210> 153
<211> 236
<212> PRT
<213> human metapneumo virus
```

```
<400> 153
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1               5                   10                  15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                  25                  30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
        35                  40                  45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
    50                  55                  60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                  70                  75                  80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
                85                  90                  95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Asp His
            100                 105                 110
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
        115                 120                 125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
    130                 135                 140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
145                 150                 155                 160
Glu Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
                165                 170                 175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
            180                 185                 190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
        195                 200                 205
Ala Ala Glu Pro Asn Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr
    210                 215                 220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Leu Ser Ser
225                 230                     235
```

```
<210> 154
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 154
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgtt caggaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 155
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 155
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgtt cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 156
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 156
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata    60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat   120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac   180
tacccaaatg aaaaagattg cgaaacaaga ggagaccatg tcttttgcga cacagcagca   240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac   300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg   360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc   420
atcaagcaac tgaacaaagg ctgctcctta                                    449


<210> 157
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 157
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata    60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat   120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac   180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca   240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac   300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg   360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc   420
atcaagcaac tgaacaaagg ctgctcctta                                    449


<210> 158
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 158
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata    60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat   120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac   180
tacccaaatg aaaaagattg cgaaacaaga ggagaccatg tcttttgcga cacagcagca   240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac   300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg   360
gctttggttg cttgctacaa gggagtgagc tgttccattg gtagcaacag agtagggatc   420
atcaagcaac tgaacaaagg ctgctcctta                                    449


<210> 159
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 159
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata    60
gacacgcctt gctggatagt aaaagcagcc ccttcttgtt cagaaaaaaa gggaaactat   120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac   180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca   240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac   300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg   360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc   420
atcaagcaac tgaacaaagg ctgctcctta                                    449


<210> 160
<211> 449
```

```
<212> DNA
<213> human metapneumo virus

<400> 160
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgtt cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449

<210> 161
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 161
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc cctcttgtt cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449

<210> 162
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 162
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc cctcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcagggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggaatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449

<210> 163
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 163
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
gacacgcctt gctggatagt aaaagcagcc cctcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449

<210> 164
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 164
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata  60
gacacgcctt gttggatagt aaaagcagcc ccttcttgct cagaaaaaaa ggggaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 165
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 165
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata  60
gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa ggggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 166
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 166
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata  60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 167
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 167
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata  60
gacacgcctt gctggatagt aaaagcggcc ccttcttgct cggaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaagatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

```
<210> 168
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 168
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gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttctattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449
```

```
<210> 169
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 169
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gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449
```

```
<210> 170
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 170
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gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449
```

```
<210> 171
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 171
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gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                   449
```

```
<210> 172
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 172
ataggagttt atggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
```

```
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 173
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 173
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gcttgcctct taagagaaga tcaagdatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 174
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 174
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gacacgcctt gctggatagt aaaagcagcc cctctcttgtt caggaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 175
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 175
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gacacgcctt gctggatagt aaaagcagcc cctctcttgtt caggaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 176
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 176
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gacacgcctt gctggatagt aaaagcggcc cctctcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac cactaattac 300
```

```
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
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<210> 177
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 177
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gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagacgaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctctggttg cttgctacaa gggagtgagc tgctccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 178
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 178
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gacacgcctt gctggatagt aaaagcggcc cctttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagacgaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
```

<210> 179
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 179
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gacacgcctt gctggatagt aaaagcggcc cctttcttgct cagaaaaaaa gggaaactat 120
gcttgcctct taagacgaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta                                    449
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<210> 180
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 180
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gacacgcctt gctggatagt aaaagcagcc cctttcttgtt caggaaaaaa gggaaactat 120
gcttgcctct taagacgaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
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atcaagcaac tgaacaaagg ctgctctta                                    449

<210> 181
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 181
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gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaa gggaaactat  120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac  180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcga cacagcagca  240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac  300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg  360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc  420
atcaagcaac tgaacaaagg ctgctctta                                    449

<210> 182
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 182
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata   60
gacacgcctt gctggatagt aaaagcagcc ccttcttgtt caggaaaaaa gggaaactat  120
gcttgcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac  180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca  240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac  300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg  360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc  420
atcaagcaac tgaacaaagg ctgctctta                                    449

<210> 183
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 183
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gacacgcctt gctggatagt aaaagcagcc ccctcttgtt ccgaaaaaaa gggaaactat  120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac  180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca  240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaaattac  300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc ccctcttggg  360
gctctggttg cttgctacaa aggagtaagc tgttccattg gcagcaatag agtagggatt  420
atcaagcagc tgaacaaagg ttgctctta                                    449

<210> 184
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 184
ataggggtct acgggagctc cgtaatttac atggtgcagc tgccaatctt tggcgttcata   60
gacacgcctt gctggatagt aaaagcagcc ccctcttgtt ccgaaaaaaa gggaaactat  120
gcttgccttt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac  180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca  240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaaattac  300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc ccctcttggg  360
gctctagttg cttgctacaa aggagtaagc tgttccattg gcagcaatag agtagggatt  420
atcaagcagc tgaacaaagg ttgctccta                                    449
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<210> 185
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 185
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gcttgccttt  taagagaaga  tcaagggtgg  tattgtcaga  atgcagggtc  aactgtttac  180
tacccaaatg  agaaagactg  tgaaacaaga  ggagaccatg  tcttttgcga  cacagtagca  240
ggaattaatg  ttgctgagca  atcaaaagag  tgcaacatca  acatatccac  tacaaattac  300
ccatgcaaag  tcagcacagg  aagacatcct  atcagtatgg  ttgcactgtc  ccctcttggg  360
gctctcagttg  cttgctacaa  aggagtaagc  tgttccattg  gcagcaatag  agtagggatc  420
atcaagcagc  tgaacaaagg  ttgctccta              449
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<210> 186
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 186
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gacacgccct  gctggatagt  aaaagcagcc  ccctcttgtt  ccgaaaaaaa  gggaaactat  120
gcttgccttt  taagagaaga  tcaagggtgg  tattgtcaga  atgcagggtc  aactgtttac  180
tacccaaatg  agaaagactg  tgaaacaaga  ggagaccatg  tcttttgcga  cacagcagca  240
ggaattaatg  ttgctgagca  atcaaaagag  tgcaacatca  acatatccac  tacaaattac  300
ccatgcaaag  tcagcacagg  aagacatcct  atcagtatgg  ttgcactgtc  ccctcttggg  360
gctctagttg  cttgctacaa  aggagtaagc  tgttccattg  gcagcaatag  agtagggatc  420
atcaagcagc  tgaacaaagg  ttgctccta              449
```

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<210> 187
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 187
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gacacgccct  gctggatagt  aaaagcagcc  ccctcttgtt  ccgaaaaaaa  gggaaactat  120
gcttgccttc  taagagaaga  ccaagggtgg  tattgtcaga  atgcagggtc  aactgtttac  180
tacccaaatg  agaaagactg  tgaaacaaga  ggagaccatg  tcttttgcga  cacagcagca  240
ggaattaatg  ttgctgagca  atcaaaggag  tgcaacatca  acatatccac  cacaaattac  300
ccatgcaaag  tcagcacagg  aaggcatcct  atcagtatgg  ttgcactgtc  ccctcttggg  360
gctctggttg  cttgctacaa  aggagtaagc  tgttctattg  gcagcaatag  agtagggatc  420
atcaagcagc  tgaacaaagg  ttgctctta              449
```

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<210> 188
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 188
atagggtct  acgggagctc  cgtaatttac  atggtgcagc  tgccaatctt  tggcgttata  60
gacacgcctt  gctggatagt  aaaagcagcc  ccctcttgtt  ccgaaaaaaa  gggaaactat  120
gcttgcctct  taagagaaga  ccaagggtgg  tattgtcaga  atgcagggtc  aactgtttac  180
tacccaaatg  agaaagactg  tgaaacaaga  ggagaccatg  tcttttgcga  cacagcagca  240
ggaattaatg  ttgctgagca  atcaaaggag  tgcaacatca  acatatccac  tacaaattac  300
ccatgcaaag  tcagcacagg  aagacatatg  atcagtatgg  ttgcactgtc  tcctcttggg  360
gctctagttg  cttgctacaa  aggagtaagc  tgttccattg  gcagcaacag  agtagggatc  420
atcaagcagc  tgaacaaagg  ttgctccta              449
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<210> 189
<211> 449
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<212> DNA
<213> human metapneumo virus

<400> 189
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gacacgcctt gctggatagt aaaagcagcc ccctcttgtt ccgaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaggactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgcactgtc ccctcttggg 360
gctctggttg cttgttacaa aggagtaagc tgttctattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctcttca   449

<210> 190
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 190
ataggggtct acgggagctc cgtaatttac atggtgcagc tgccaatctt tggcgttata 60
gacacgcctt gctggatagt aaaagcagcc ccctcttgtt ccgaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
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atcaagcagc tgaacaaagg ttgctcttca   449

<210> 191
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 191
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gacacgcctt gctggatagt aaaagcagcc ccctcttgtt ccgaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctctggttg cttgctacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctcttca   449

<210> 192
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 192
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gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
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gctctggttg cctgttacaa aggagtaagt tgttccattg gcagcaatag agtagggatc 420
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<210> 193
<211> 449
<212> DNA
<213> human metapneumo virus

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gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
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gctctggttg cttgctacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
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<210> 194
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 194
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gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
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gctctggttg cttgctacaa aggagtaagt tgttccattg gcagcaatag agtagggatc 420
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<210> 195
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 195
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gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
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gctctggttg cttgctacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta                                    449

<210> 196
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 196
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gacacgcctt gctggatagt aaaagcagcc ccttcttgtt ccgaaaaaa gggaaattat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaaacaaga ggagaccatg tcttttgcga cacagcagca 240
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gctctggttg cttgctacaa aggagtaagt tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta                                    449

<210> 197
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 197
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gctctcggttg cttgctacaa aggagtaagc tgttccattg gcagcaacag agtaggggatc 420
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```

<210> 198
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 198
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
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gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

<210> 199
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 199
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gatacacctt gttggatcat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc tactgtttac 180
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ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaattg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
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<210> 200
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 200
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gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

<210> 201
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 201
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gatacacctt gttggatcat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc tactgtttac 180
```

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gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                   449
```

```
<210> 202
<211> 449
<212> DNA
<213> human metapneumo virus
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```
<400> 202
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gcttgcctcc taagagagga tcaaggtgg tattgcaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
```

```
<210> 203
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 203
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaaggtgg tattgcaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
```

```
<210> 204
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 204
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaaggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
```

```
<210> 205
<211> 449
<212> DNA
<213> human metapneumo virus
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```
<400> 205
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gcttgcctcc taagagagga tcaaggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
```

```
ccatgcaaag tcagcacagg aagacactct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
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<210> 206
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 206
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
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ccatgcaaag tcagcacagg aagacactct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
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<210> 207
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 207
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttttac 180
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ccatgcaaag tcagcacagg aagacactct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
```

<210> 208
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 208
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gatacacctt gttggataat caaggcagct cagaaaaaaa cgggaattat 120
gcttgcctcc taagagagga tcaagggtgg tactgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
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ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata                                   449
```

<210> 209
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 209
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gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
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ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
```

91

```
atcaaacaat tacccaaagg ctgctcata                                    449
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```
<210> 210
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 210
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gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tgttttgtga cacagcagca 240
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gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatt 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

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<210> 211
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 211
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gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tgttttgtga cacagcagca 240
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gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

```
<210> 212
<211> 449
<212> DNA
<213> human metapneumo virus
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```
<400> 212
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gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
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gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

```
<210> 213
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 213
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gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
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gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacccaaagg ctgctcata                                    449
```

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<210> 214
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 214
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gatacacctt gttggataat caaggcagct ccctcttgct cagagaaaaa cgggaattat     120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac     180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tgttttgtga tacagcagca     240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac     300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt     360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc     420
atcaaacaat tacctaaagg ctgctcata                                       449

<210> 215
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 215
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat     120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atcaggatc cactgtttac     180
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gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac     300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt     360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc     420
atcaaacaat tacccaaagg ctgctcata                                       449

<210> 216
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 216
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gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat     120
gcttgcctcc taagagagga tcaagggtgg tactgtaaaa atgcaggatc cactgtttac     180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga tacagcagca     240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac     300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt     360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc     420
atcaaacaat tacctaaagg ctgctcata                                       449

<210> 217
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 217
ataggggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tggtgtcata      60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat     120
gcttgcctcc taagagagga tcaagggtgg tattgcaaaa atgcaggatc cactgtttac     180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga tacagcagca     240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac     300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt     360
gctttggtag cttgctacaa gggggttagc tgctcgattg gcagtaatcg ggttggaata     420
atcaaacaac tacctaaagg ctgctcata                                       449

<210> 218
<211> 449
```

```
<212> DNA
<213> human metapneumo virus

<400> 218
atagggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac  300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa agggggttagc tgctcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                    449
```

```
<210> 219
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 219
atagggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac  300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa agggggttagc tgctcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                    449
```

```
<210> 220
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 220
atagggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga ccaagggtgg tattgtaaaa atgcgggatc cactgtttac  180
tacccaaatg aaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac  300
ccatgcaaag tcagcacagg aagacacccct atcagcatgg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa agggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                    449
```

```
<210> 221
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 221
atagggtct acggaagctc cgtgatttac atggtccagc taccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagctgca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac  300
ccatgcaaag tcagcacagg aagacacccct atcagcatgg ttgcactgtc acctctcggc  360
gctttggtag cttgctacaa agggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                    449
```

```
<210> 222
<211> 449
<212> DNA
<213> human metapneumo virus
```

<400> 222

```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaaggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac  300
ccatgcaaag tcagcacagg aagacaccct atcagcatg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                   449
```

<210> 223
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 223

```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaaggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaaagactg tgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac  300
ccatgcaaag tcagcacagg aagacaccct atcagcatg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                   449
```

<210> 224
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 224

```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga ccaaggtgg tattgtaaaa atgcgggatc cactgtttac  180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac  300
ccatgcaaag tcagcacagg aagacaccct atcagcatg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                   449
```

<210> 225
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 225

```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat  120
gcttgcctcc taagagagga tcaaggtgg tattgtaaaa atgcaggatc cactgtttac  180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca  240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac  300
ccatgcaaag tcagcacagg aagacaccct atcagcatg ttgcactatc acctctcggt  360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata  420
atcaaacaac tacctaaagg ctgctcata                                   449
```

<210> 226
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 226

```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata   60
```

```
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaaggggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                     449
```

<210> 227
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 227
```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcaattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                     449
```

<210> 228
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 228
```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttccaattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                     449
```

<210> 229
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 229
```
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa gggggttagc tgttccgattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                     449
```

<210> 230
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 230
```
ataggggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
```

```
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactgtc acctctcggc 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                   449
```

```
<210> 231
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 231
ataggggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaacg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactat 300
ccgtgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                   449
```

```
<210> 232
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 232
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcaattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                   449
```

```
<210> 233
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 233
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga tgcaacatca acatatctac aaccaactac 240
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaata 420
atcaaacaac tacctaaagg ctgctcata                                   449
```

```
<210> 234
<211> 149
<212> PRT
<213> human metapneumo virus
```

```
<400> 234
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
```

```
            35                      40                     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                    85                      90                     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                    140
Asn Lys Gly Cys Ser
145


<210> 235
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 235
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                       5                      10                     15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                      25                     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                    85                      90                     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                    140
Asn Lys Gly Cys Ser
145


<210> 236
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 236
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                       5                      10                     15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                      25                     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
```

```
                        85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
                115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 237
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 237
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
                115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 238
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 238
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
                115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
```

```
     130                          135                     140
Asn Lys Gly Cys Ser
145


<210> 239
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 239
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Gly Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 240
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 240
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Gly Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 241
```

```
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 241
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145


<210> 242
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 242
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145


<210> 243
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 243
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
```

```
 1                    5                    10                   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                 20                   25                   30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
             35                   40                   45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
         50                   55                   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                   70                   75                   80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                 85                   90                   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                 100                  105                  110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
             115                  120                  125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
         130                  135                  140
Asn Lys Gly Cys Ser
145
```

<210> 244
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 244
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1                    5                    10                   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                 20                   25                   30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
             35                   40                   45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
         50                   55                   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                   70                   75                   80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                 85                   90                   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                 100                  105                  110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
             115                  120                  125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
         130                  135                  140
Asn Lys Gly Cys Ser
145
```

<210> 245
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 245
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1                    5                    10                   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                 20                   25                   30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
             35                   40                   45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
```

102

```
     50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                    85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 246
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 246
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                       5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                    20                      25                      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                    85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 247
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 247
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                       5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                    20                      25                      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Arg Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                    85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
```

```
                100                    105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                    135                    140
Asn Lys Gly Cys Ser
145


<210> 248
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 248
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                      10                     15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                     25                     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                     40                     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                     55                     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                     70                     75                     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                     90                     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                    105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                    135                    140
Asn Lys Gly Cys Ser
145


<210> 249
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 249
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                      10                     15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                     25                     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                     40                     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                     55                     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                     70                     75                     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                     90                     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                    105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                    135                    140
Asn Lys Gly Cys Ser
```

145

```
<210> 250
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 250
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 251
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 251
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 252
<211> 149
<212> PRT
```

<213> human metapneumo virus

<400> 252
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1   5   10   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20   25   30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35   40   45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50   55   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65   70   75   80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85   90   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100   105   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115   120   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130   135   140
Asn Lys Gly Cys Ser
145

<210> 253
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 253
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1   5   10   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20   25   30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35   40   45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50   55   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65   70   75   80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85   90   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100   105   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115   120   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130   135   140
Asn Lys Gly Cys Ser
145

<210> 254
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 254
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1   5   10   15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser

```
                20                  25                  30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 255
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 255
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 256
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 256
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
```

```
       65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                        85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                   135                   140
Asn Lys Gly Cys Ser
145
```

<210> 257
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 257

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                    25                    30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                    40                    45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                        85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                   135                   140
Asn Lys Gly Cys Ser
145
```

<210> 258
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 258

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                    25                    30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                    40                    45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                        85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
```

```
              115                    120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                   140
Asn Lys Gly Cys Ser
145


<210> 259
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 259
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145


<210> 260
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 260
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145
```

```
<210> 261
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 261
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65              70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 262
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 262
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65              70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 263
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 263
```

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145
```

```
<210> 264
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 264
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145
```

```
<210> 265
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 265
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
```

```
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Val Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145
```

<210> 266
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 266

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145
```

<210> 267
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 267

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
```

112

```
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                 135                 140
Asn Lys Gly Cys Ser
145
```

<210> 268
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 268
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                 135                 140
Asn Lys Gly Cys Ser
145
```

<210> 269
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 269
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                 135                 140
```

```
Asn Lys Gly Cys Ser
145


<210> 270
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 270
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 271
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 271
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Asn Lys Gly Cys Ser
145


<210> 272
<211> 149
```

```
<212> PRT
<213> human metapneumo virus

<400> 272
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145


<210> 273
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 273
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145


<210> 274
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 274
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                   10                  15
```

```
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20                      25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
  50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                  85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
              100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 275
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 275
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1                   5                     10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20                      25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
  50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                  85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
              100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                     135                     140
Asn Lys Gly Cys Ser
145


<210> 276
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 276
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1                   5                     10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20                      25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                      40                      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
  50                      55                      60
```

116

```
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145
```

```
<210> 277
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 277
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Asn Lys Gly Cys Ser
145
```

```
<210> 278
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 278
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
```

```
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145
```

```
<210> 279
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 279
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Trp Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145
```

```
<210> 280
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 280
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145
```

```
<210> 281
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 281
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 282
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 282
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 283
<211> 149
<212> PRT
<213> human metapneumo virus
```

<400> 283
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
            130                 135                 140
Pro Lys Gly Cys Ser
145
```

<210> 284
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 284
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
            130                 135                 140
Pro Lys Gly Cys Ser
145
```

<210> 285
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 285
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
```

```
                35                      40                      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Ser Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Pro Lys Gly Cys Ser
145


<210> 286
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 286
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                     135                     140
Pro Lys Gly Cys Ser
145


<210> 287
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 287
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
```

```
                        85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                   100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
               115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
           130                     135                     140
Pro Lys Gly Cys Ser
145


<210> 288
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 288
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                    85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                   100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
               115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
           130                     135                     140
Pro Lys Gly Cys Ser
145


<210> 289
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 289
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                       10                      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                      25                      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                      55                      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                      75                      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                    85                      90                      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                   100                     105                     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
               115                     120                     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
```

```
    130                    135                   140
Pro Lys Gly Cys Ser
145


<210> 290
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 290
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                  10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 291
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 291
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1               5                  10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 292
```

```
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 292
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Pro Lys Gly Cys Ser
145


<210> 293
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 293
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                     140
Pro Lys Gly Cys Ser
145


<210> 294
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 294
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
```

```
    1               5                      10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                      25                    30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                      90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                     135                   140
Pro Lys Gly Cys Ser
145
```

<210> 295
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 295
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                      10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                      25                    30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                      55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                      70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                      90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                     105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                     120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                     135                   140
Pro Lys Gly Cys Ser
145
```

<210> 296
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 296
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                      10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                      25                    30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                      40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
```

```
     50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
            85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                   135                   140
Pro Lys Gly Cys Ser
145
```

<210> 297
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 297
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                     5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                    40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
            85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                   135                   140
Pro Lys Gly Cys Ser
145
```

<210> 298
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 298
```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                     5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                    40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
            85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
```

```
                 100                    105                    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
145


<210> 299
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 299
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
           20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                    40                  , 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
              85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
145


<210> 300
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 300
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
           20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                    40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
              85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
```

145

```
<210> 301
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 301
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 302
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 302
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 303
<211> 149
<212> PRT
```

```
<213> human metapneumo virus

<400> 303
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 304
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 304
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 305
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 305
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
```

```
                20                   25                   30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                   40                   45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                   55                   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                   70                   75                   80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                   90                   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                  105                  110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                  120                  125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                  135                  140
Pro Lys Gly Cys Ser
145
```

```
<210> 306
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 306
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                   25                   30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                   40                   45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                   55                   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                   70                   75                   80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                   90                   95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                  105                  110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                  120                  125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                  135                  140
Pro Lys Gly Cys Ser
145
```

```
<210> 307
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 307
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                   25                   30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                   40                   45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                   55                   60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
```

```
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                    85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                   135                   140
Pro Lys Gly Cys Ser
145


<210> 308
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 308
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                    40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                    85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
            115                   120                   125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
        130                   135                   140
Pro Lys Gly Cys Ser
145


<210> 309
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 309
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1                   5                     10                    15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20                    25                    30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
            35                    40                    45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
        50                    55                    60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                    70                    75                    80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                    85                    90                    95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100                   105                   110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
```

```
            115                    120                    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
145


<210> 310
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 310
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
145


<210> 311
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 311
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
            85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                    135                    140
Pro Lys Gly Cys Ser
145
```

```
<210> 312
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 312
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 313
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 313
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1               5                   10                  15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
            20                  25                  30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
        35                  40                  45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
    50                  55                  60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                  70                  75                  80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85                  90                  95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
            100                 105                 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
        115                 120                 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
    130                 135                 140
Pro Lys Gly Cys Ser
145


<210> 314
<211> 539
<212> PRT
<213> human metapneumo virus

<400> 314
```

```
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1               5                   10                  15
His Gly Leu Lys Glu Ser Tyr Leu Glu Gln Ser Cys Ser Thr Ile Thr
                20                  25                  30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
            35                  40                  45
Thr Leu Glu Val Gly Asp Val Gln Asn Leu Thr Cys Ala Asp Gly Pro
50                  55                  60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
            180                 185                 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
            420                 425                 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
        435                 440                 445
Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
                485                 490                 495
```

134

```
Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
            500                 505                 510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
        515                 520                 525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
    530                 535


<210> 315
<211> 539
<212> PRT
<213> human metapneumo virus

<400> 315
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1               5                  10                  15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
    50                  55                  60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Thr Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
                165                 170                 175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
            180                 185                 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Thr Val Gln
            260                 265                 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
        275                 280                 285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
    290                 295                 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
            340                 345                 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380
```

135

```
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
            420                 425                 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
        435                 440                 445
Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460
Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                 470                 475                 480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
                485                 490                 495
Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
            500                 505                 510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
    515                 520                 525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Ser
    530                 535
```

```
<210> 316
<211> 539
<212> PRT
<213> human metapneumo virus

<400> 316
Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
1                   5                   10                  15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
                20                  25                  30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
    50                  55                  60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Gln Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
                165                 170                 175
Ile Asn Arg Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
            180                 185                 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
        195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
    210                 215                 220
Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
            260                 265                 270
```

```
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
        275                     280                 285
Ala Pro Ser Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg
    290                     295                 300
Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
305                     310                 315                 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
                325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
            340                 345                 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
        355                 360                 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
    370                 375                 380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Trp Val Gly Ile Ile
385                 390                 395                 400
Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                405                 410                 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
            420                 425                 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
        435                 440                 445
Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
    450                 455                 460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
465                 470                 475                 480
Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Val Ile
                485                 490                 495
Leu Val Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
            500                 505                 510
Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
        515                 520                 525
Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
    530                 535
```

<210> 317
<211> 539
<212> PRT
<213> human metapneumo virus

<400> 317
```
Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
1               5                   10                  15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
            20                  25                  30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
        35                  40                  45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
    50                  55                  60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                  70                  75                  80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                85                  90                  95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
            100                 105                 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
        115                 120                 125
Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Thr Thr
    130                 135                 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                 150                 155                 160
```

137

```
Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
              165                 170                 175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
          180                 185                 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
      195                 200                 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
  210                 215                 220
Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
225                 230                 235                 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
              245                 250                 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
          260                 265                 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
      275                 280                 285
Ala Pro Ser Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
  290                 295                 300
Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
305                 310                 315                 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
              325                 330                 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
          340                 345                 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
      355                 360                 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370                 375                 380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                 390                 395                 400
Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
              405                 410                 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
          420                 425                 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
      435                 440                 445
Ile Arg Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
  450                 455                 460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
465                 470                 475                 480
Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
              485                 490                 495
Leu Ile Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
          500                 505                 510
Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
      515                 520                 525
Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
      530                 535
```

```
<210> 318
<211> 1620
<212> DNA
<213> human metapneumo virus

<400> 318
atgtcttgga aagtggtgat catttttca ttgttaataa cacctcaaca cggtcttaaa  60
gagagctact tagaagagtc atgtagcact ataactgaag gatatctcag tgttctgagg 120
acaggttggt acaccaatgt ttttacactg gaggtaggcg atgtagagaa ccttacatgt 180
gccgatggac ccagcttaat aaaaacgaa ttagacctga ccaaaagtgc actaagagag 240
ctcagaacag tttctgctga tcaactggca agagaggacg aaattgaaaa tcccagacaa 300
tctagattcg ttctaggagc aatagcactc ggtgttgcaa ctgcagctgc agttacagca 360
```

138

```
ggtgttgcaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
ctcaaaaaga ccaatgaagc agtatcctaca ttggggaatg gagttcgtgt gttggcaact 480
gcagtgagag agctgaaaga ttttgtgagc aagaatctaa cacgtgcaat caacaaaaac 540
aagtgcgaca ttgctgacct gaaaatggcc gttagcttca gtcaattcaa cagaaggttc 600
ctaaatgttg tgcggcaatt ttcagacaac gctgaataca caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagagct gtttccaaca tgctaacatc tgcaaggcaa 720
ataaaactga tgttgaggaa ccgtgcgatg gtaagaagaa aagggttcgg aatcctgata 780
ggagtttacg gaagctccgt aattacatg gtgcaactgc caatctttgg gattatagac 840
acgccttgct ggatagtaaa agcagcccct tcttgttcag gaaaaaaggg aaactatgct 900
tgcctcttaa ggagaagacca aggatggtat tgtcaaaatg cagggtcaac tgtttactac 960
ccaaatgaaa aagactgtga aacaagagga gaccatgtct tttgcgacac agcagcagga 1020
atcaatgttg ctgagcagtc aaaggagtgc aacataaaca tatctactac taatttaccca 1080
tgcaaagtta gcacaggaag acatcctatc agtatggttg cactatctcc tcttggggct 1140
ttggttgctt gctacaaggg agtgagctgt tccattggca gcaacagagt agggatcatc 1200
aagcaactga acaaaggctg ctctttatata accaaccaag acgcagacac agtgacaata 1260
gacaacactg tatccagct aagcaaagtt gaaggcgaac agcatgttat aaaaggcaag 1320
ccagtgtcaa gcagctttga cccagtcaag ttctctgaag atcaattcaa tgttgcactt 1380
gaccaagttt tcgagagcat tgagaacagt caggccttag tgcagctttg tgatcaatc aaacagatt 1440
ctaagcagtg cagagaaagg aaacactggc ttcatcattg taataattct aatgctctgtc 1500
cttggctcta ccatgatcct agtgagtgtt ttttatcatta taaagaaaac aaagaaaaccc 1560
acaggagcac ctccagagct gagtggtgtc acaaacaatg gcttcatacc acataattag 1620
```

<210> 319
<211> 1620
<212> DNA
<213> human metapneumo virus

<400> 319

```
atgtcttgga aagtggtgat cattttttca ttgctaataa cacctcaaca cggtcttaaa 60
gagagctacc tagaagaatc atgtagcact ataactgagg gatatcttag tgttctgagg 120
acaggttgt ataccaacgt ttttacatta gaggtgggtg atgtagaaaa ccttacatgt 180
tctgatggac ctagcctaat aaaaacagaa ttagatctga ccaaagtgc actaagagag 240
ctcaaaacag tctctgctga ccaattggca agagaggaac aaattgagaa tcccagacaa 300
tctaggtttg ttctaggagc aatagcactc ggttgttgcaa cagcagctgc agtcacagca 360
ggtgttgcaa ttgccaaaac catccggctt gagagtgaag tcacagcaat taagaatgcc 420
ctcaaaacga ccaatgaagc agtatcctaca ttggggaatg gagttcgagt gttggcaact 480
gcagtgagag agctaaaaga ctttgtgagc aagaatttaa ctcgtgcaat caacaaaaac 540
aagtgcgaca ttgctgacct aaaaatggct gttagcttca gtcaattcaa cagaaggttt 600
ctaaatgttg tgcggcaatt ttcagacaac gctgaataca caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagagct gtttccaaca tgctaacaca ctcaaggcaa 720
ataaaattga tgttggagaa ccgtgcgatg gtgcgaagaa aggggttccg aatcctgatt 780
ggggtctacg ggagctccgt aattacacg gtgcagctgc caatctttgg cgttatagac 840
acgccttgct ggatagtaaa agcagcccct tcttgttccg aaaaaaggg aaactatgct 900
tgcctcttaa gagaagacca aggtggtat tgtcagaatg cagggtcaac tgtttactac 960
ccaaatgaga aagactgtga aacaagagga gaccatgtct tttgcgacac agcagcagga 1020
attaatgttg ctgagcaatc aaaggagtgc aacatacaca tatccactac taatttaccca 1080
tgcaaagtta gcacaggaag acatcctatc agtatggttg cactgtctcc tcttggggct 1140
ttggttgctt gctacaaagg tgtctctata taccaaccaag atgcagacac agtgacaata 1260
gacaacactg tatatcagct aagcaaagtt gaggtgaac agcatgttat aaaaggcaag 1320
ccagtgtcaa gcagctttga tccaatcaag tttctgaag atcaattcaa tgttgcactt 1380
gaccaagttt ttgagaacat tgaaacagc caggccttag tagtcaatc aaacagaatt 1440
ctaagcagtg cagagaaagg aatactggc ttatcattg taataattct aattgctgtc 1500
cttggctcta gcatgatcct agtgagcatc ttcattataa tcaagaaaac aaagaaacca 1560
acgggagcac ctccagagct gagtggtgtc acaaacaatg gcttcatacc acacagttag 1620
```

<210> 320
<211> 1620
<212> DNA
<213> human metapneumo virus

```
<400> 320
atgtcttgga aagtgatgat catcatttcg ttactcataa caccccagca cgggctaaag   60
gagagttatt tggaagaatc atgtagtact ataactgagg gatacctcag tgttttaaga  120
acaggctggt acactaatgt cttcacatta gaagttggtg atgttgaaaa tcttacatgt  180
actgatggac ctagcttaat caaaacagaa cttgacctaa ccaaaagtgc tttaaggcaa  240
ctcaaaacag tcttctgctga tcagttggcg agagaagag aaattgaaaa tcccaagcaa  300
tcaagatttg tcttagtgtc gatagctctc ggagttgcta cagcagcagc agtcacagca  360
ggcattgcaa tagccaaaac cataaggctt gagagtgagg tgaatgcaat taaagtgct  420
ctcaaaacaa ctaatgaagc agtatccaca ttaggaatg gtgtgcggt cctagccact  480
gcagtgagag agctaaaaga atttgtgagc aaaaacctga ctagtgcaat caacaggaac  540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattt  600
ctaaatgttg tgcggcagtt ttcagacaat gcaggggataa caccagcaat atcattgacc  660
ctgatgactg atgctgagtt ggcagagagct gtatcataca tgccaacatc tgcagggcag  720
ataaaactga tgttggagaa ccgtgcaatg gtaaggagaa aaggatttg aatcctgata  780
gggtctacg gaagctctgt gattcatg gttcaattgc cgatctttgg tgtcatagat  840
acaccttgtt ggataatcaa ggcagctccc tcttgctcag aaaaaaacgg gaattatgct  900
tgcctcctaa gagaggatca aggtggtat tgtaaaaatg caggatctac tgtttactac  960
ccaaatgaaa aagactgcga aacaaggagg gatctgtt tttgtgacac agacagcagg 1020
atcaatgttg ctgagcaatc aagagaatgc aacatcaaca tatctaccac caactaccca 1080
tgcaaagtca gcacaggaag acaccctatc agcatggttg cactatcacc tctcggtgct 1140
ttggtggctt gctataaagg ggtaagctgc tcgattggca gcaattgggt tggaatcatc 1200
aaacaattac ccaaaaggctg ctcatacata accaccagg atgcagacac tgtaacaatt 1260
gacaataccg tgtatcaact aagcaaagtt gaagctgtaa aaaacaggga 1320
ccagtttcaa gcagtttttga tccaatcaag tttcctgagg atcagttcaa tgttgcgctt 1380
gatcaagtct tcgaaagcat tgagaaacagt caggcactag tggaccagtc aaacaaaatt 1440
ctaaacagtg cagaaaaaag aaacactggt ttcattatcg tagtaatttt ggttgctgtt 1500
cttggtctaa ccatgattc agtgagcatc atcatcataa tcaagaaaac aaggaagccc 1560
acaggagcac ctccagagct gaatggtgtc accaacggcg gtttcataac acatagttug 1620
```

```
<210> 321
<211> 1620
<212> DNA
<213> human metapneumo virus
```

```
<400> 321
atgtcttgga aagtgatgat tatcatttcg ttactcataa cacctcagca cggactaaaa   60
gaaagttatt tagaagaatc atgtagtact ataactgagg gatatctcag tgttttaaga  120
acaggttggt acaccaatgt cttcacatta gaagttggtg atgttgaaaa tcttacatgt  180
actgatggac ctagcttaat caaaacagaa ccaaaagtgc tctgagagaa atacagttt  240
ctcaaaacag tttctgctga tcagttaggcg agagaagaac aaattgaaaa tcccaagcaa  300
tcaaggtttg tcctaggtgc aatagctctt ggagttgcca cagcagcagc agtcacagca  360
ggcattgcaa tagccaaaac cataaggctt gagagtgagg tgaatgcaat caaaggtgct  420
ctcaaaacaa ccaacgaggc agtatccaca ttaggaaatg gtgtgcggt cctaccacct  480
gcagtgagag agctaaaaga atttgtgagc aaaaacctga ctagtgcaat caacaaggac  540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa caaaagaatc  600
ctaaatgtag tgcggcagtt ttcagacaat gcaggggataa caccagcaat atcattgaac  660
ctaataactg atgctgagtt ggcagagagct gtatcataca tgccaacatc tgcaggacag  720
ataaaactaa tgttagaaga ccgtggcaatg gtgaggagaa aaggatttg gatctcttgg  780
gggtctacgg aagctctgt gatttcatg gtccagctgc cgatctttgg tgtcatagat  840
acaccttgtt ggataatcaa ggcagctccc tcttgttcag aaaaagatgg aaattatgct  900
tgcctcctaa gagaggatca aggtggtat tgtaaaaatg caggatccac tgtttactac  960
ccaaatgaaa aagactgcga aacaaggagg gatctgtgac agacagcagg 1020
atcaatgttg ctgagcaatc aagagaatgc aacatcaaca tatctaccac caactaccca 1080
tgcaaagtca gcacaggaag acaccctatc agcatggttg cactatcacc tctcggtgct 1140
ttggtagctt gctacaaggg ggttactgc tcgattggca gtaatcgggt tggaataatc 1200
aaacaactac ctaaaggctg ctcatacata actaccaggg acgcagacac tgtaacaatt 1260
gacaacaactg tgtatcaact aagcaaagtt gaagctgtaa aaaacaggga 1320
ccagtttcaa gcagtttttga tccaatcaag tttcctgagg atcagttcaa tgttgcgctt 1380
gatcaagtct tcgaaagcat tgagaaacagt caagcactag tggaccagtc aaacaaaatt 1440
ctgaacagtg cagaaaaaag aaacactggt ttcattattg taataatttt gattgctgtt 1500
cttgggttaa ccatgattc agtgagcatc atcatcataa tcaaaaaaac aaggaagccc 1560
```

acaggggcac ctccagagct gaatggtgtt accaacggcg gttttatacc gcatagttag 1620

<210> 322
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 322
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1   5   10   15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20   25   30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35   40   45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
    50   55   60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65   70   75   80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
                85   90   95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
            100   105   110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
        115   120   125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
    130   135   140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145   150   155   160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
                165   170   175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
            180   185   190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
        195   200   205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
    210   215   220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225   230   235

<210> 323
<211> 219
<212> PRT
<213> human metapneumo virus

<400> 323
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1   5   10   15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
            20   25   30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
        35   40   45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
    50   55   60
His Thr Ser Ser Pro Pro Thr Glu Pro Asn Lys Glu Ala Ser Thr Ile
65   70   75   80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Ser Ser Gln His Pro Thr Gln
                85   90   95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
            100   105   110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser

```
          115                    120                    125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
    130                    135                    140
Lys Pro Thr Val His Thr Ile Asn Asn Pro Asn Thr Ala Ser Ser Thr
145                    150                    155                    160
Gln Ser Pro Pro Arg Thr Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
                   165                    170                    175
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Leu Val Gln
            180                    185                    190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
            195                    200                    205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn
    210                    215


<210> 324
<211> 224
<212> PRT
<213> human metapneumo virus

<400> 324
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1                  5                     10                     15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
            20                     25                     30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
            35                     40                     45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
    50                     55                     60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65                     70                     75                     80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
            85                     90                     95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro Glu Gly His
            100                    105                    110
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala Pro Gln Gln
    115                    120                    125
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn Glu Gln Ile
    130                    135                    140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr Gln Lys
145                    150                    155                    160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
                   165                    170                    175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
            180                    185                    190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Gln Ser Ser
            195                    200                    205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro His His Ala
    210                    215                    220


<210> 325
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 325
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1                  5                     10                     15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
            20                     25                     30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
```

```
              35                    40                    45
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His
   50                    55                    60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65                    70                    75                    80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
              85                    90                    95
Leu Ala Ala Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
             100                   105                   110
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
             115                   120                   125
Thr Thr Asp Glu Tyr Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
          130                   135                   140
Thr Gln Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145                   150                   155                   160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
             165                   170                   175
Thr Thr Asn Gln Thr Ser Tyr Val Arg Gln Ala Thr Thr Thr Ser Ala
             180                   185                   190
Arg Ser Arg Asn Ser Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
          195                   200                   205
Ala Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
   210                   215                   220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225                   230                   235
```

```
<210> 326
<211> 708
<212> DNA
<213> human metapneumo virus

<400> 326
gaggtgaaag tggagaacat tcgaacaata gatatgctca aagcaagagt aaaaaatcgt   60
gtggcacgca gcaaatgctt taaaaatgcc tctttggtcc tcataggaat aactacattg  120
agtattgccc tcaatatcta tctgatcata aactataaaa tgcaaaaaaa cacatctgaa  180
tcagaacatc acaccagctc atcacccatg gaatccagca gagaaactcc aacggtcccc  240
acagacaact cagacaccaa ctcaagccca cagcatccaa ctcaacagtc cacagacagg  300
tccacactct actttgcagc ctcagcaagc tcaccagaga cagaaccaac atcaacacca  360
gatcaacaa accgcccgcc cttcgtcgac acacacacaa caccaccaag cgcaagcaga  420
acaaagacaa gtccggcagt ccacacaaaa aacaacccaa ggacaagtc tagaacacat  480
tctccaccac gggcaacgac aaggacggca cgcagaacca ccactctccg cacaagcagc  540
acaagaaaga gaccgtccac agcatcagtc caacctgaca tcagcgcaac aacccacaaa  600
aacgaagaag caagtccagc gagcccacaa acatctgcaa gcacaacaag aatacaaagg  660
aaaagcgtgg aggccaacac atcaacaaca tacaaccaaa ctagttaa             708
```

```
<210> 327
<211> 660
<212> DNA
<213> human metapneumo virus

<400> 327
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat   60
cgtgtggcac gtagcaaatg cttttaaaaat gcttctttaa tcctcatagg aataactaca  120
ctgagtatag ctctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatcc  180
gaatcagaac accacaccag ctcaccaccc acagaaccca acaaggaagc ttcaacaatc  240
tccacagaca acccagacat caatccaagc tcacagcatc caactcaaca gtccacagaa  300
aaccccacac tcaacccgc agcatcagcg agcccatcag aaacagaacc agcatacaca  360
ccagacacaa caaccgcct gtcctccgta gacaggtcca cagcacaacc cagcaagaag  420
agaacaaaga caaaaccgac agtccacaca atcaacaacc caacacagc ttccagtaca  480
caatccccac cacggacaac aacgaaggca atccgcaagc ccactctt ccgcatgagc  540
agcacaggaa aaagaccaac cacaacatta gtccagtccg acagcagcac cacaacccaa  600
```

```
aatcatgaag aaacaggttc agcgaaccca caggcgtctg caagcacaat gcaaaactag 660
```

```
<210> 328
<211> 675
<212> DNA
<213> human metapneumo virus

<400> 328
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat tttcctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa actgtgctaa catgcgtctg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacagag 300
aactcaacat ccccagtagc aaccccagag ggccatccat acacagggac aactcaaaca 360
tcagacacaa cagctcccca gcaaaccaca gacaaacaca cagcaccgct aaaatcaacc 420
aatgaacaga tcaccccagac aaccacagag aaaaagacaa tcagagcaac aacccaaaaa 480
agggaaaaag gaaaagaaaa cacaaaccaa accacagacca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagt gagacaatca caacatccga cagacccaga 600
actgacacca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
ccacaccatg catg                                                   675
```

```
<210> 329
<211> 711
<212> DNA
<213> human metapneumo virus

<400> 329
atggaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa aatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ttaagtatgg cacttaatat tttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggaac actgtgttaa tatgcgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacaa caaacccaat ccacagcagg caacacagtt ggccgcagag 300
gattcaacat ctctagcaga aacctcagaa gaccatctac acacagggac aactcaaaca 360
ccagtgcaa cagtctctca gcaaaccaca gacgagtaca caacattgct gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa ccggagcaac aaccaaaaa 480
gaaaccacaa ctcgaactac aagcacagct gcaacccaaa cactcaacac taccaaccaa 540
actagctatg tgagagaggc aaccacaaca tccgccagat ccagaaacag tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaaccaca ccatccacag 660
aaaagcacaa caacaacata caacacagac acatcctctc caagtagtta a          711
```

```
<210> 330
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 330
Met Asp Pro Leu Asn Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1               5                   10                  15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
            20                  25                  30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
        35                  40                  45
Ala Ile Glu Asn Pro Val Ile Glu His Val Arg Leu Lys Asn Ala Val
    50                  55                  60
Asn Ser Lys Met Lys Ile Ser Asp Tyr Lys Ile Val Glu Pro Val Asn
65                  70                  75                  80
Met Gln His Glu Ile Met Lys Asn Val His Ser Cys Glu Leu Thr Leu
                85                  90                  95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Thr Leu Lys Leu
            100                 105                 110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asp Thr
```

```
                 115                       120                     125
     Ser Ile Leu Ser Phe Ile Asp Val Glu Phe Ile Pro Ser Trp Val Ser
         130                       135                     140
     Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
     145                       150                     155                 160
     Arg Lys Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
                         165                       170                 175
     Gly Lys Leu Val Phe Val Val Ser Ser Tyr Gly Cys Ile Val Lys Ser
                     180                       185                 190
     Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
                 195                       200                 205
     Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
             210                       215                 220
     Val Ser Asn Ser Leu Asn Glu Asn Gln Glu Gly Leu Gly Leu Arg Ser
     225                       230                 235                 240
     Asn Leu Gln Gly Ile Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
                     245                       250                 255
     Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
                 260                       265                 270
     Glu Gly Phe Ile Met Ser Glu Ile Leu Arg Ile Thr Glu Ile Ala Gln
             275                       280                 285
     Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Asp Gln
     290                       295                 300
     Leu Thr Lys Leu Lys Asn Lys Asn Arg Leu Arg Val His Gly Thr Val
     305                       310                 315                 320
     Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
                         325                       330                 335
     Gly Asp Thr Leu Arg Cys Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
                     340                       345                 350
     Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
             355                       360                 365
     Val Asp Glu Arg Asp Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
         370                       375                 380
     Thr Lys Ile Leu Arg Trp Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
     385                       390                 395                 400
     Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
                         405                       410                 415
     Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Thr Met Tyr Phe
                     420                       425                 430
     Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Glu Gln Asp Phe
             435                       440                 445
     Leu Glu Leu Ala Ala Ile Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
         450                       455                 460
     Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
     465                       470                 475                 480
     Lys Arg Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Lys
                     485                       490                 495
     Ile Lys Asn Arg Tyr Leu Glu Glu Thr Phe Asn Ala Ser Asp Ser Leu
             500                       505                 510
     Lys Thr Arg Arg Val Leu Glu Tyr Tyr Leu Lys Asp Asn Lys Phe Asp
         515                       520                 525
     Gln Lys Glu Leu Lys Ser Tyr Val Val Lys Gln Glu Tyr Leu Asn Asp
     530                       535                 540
     Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
     545                       550                 555                 560
     Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
                 565                       570                 575
     Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
             580                       585                 590
     Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
         595                       600                 605
     Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Arg Asn Asp Ser Tyr Asn
```

```
            610                    615                    620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
625                    630                    635                    640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
                  645                    650                    655
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
              660                    665                    670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
          675                    680                    685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr
      690                    695                    700
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
705                    710                    715                    720
Met Glu Ala Ile Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Cys
                  725                    730                    735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
              740                    745                    750
Lys Pro Val Lys Leu Ser Glu Gly Leu Asp Glu Val Lys Ala Asp Tyr
          755                    760                    765
Ser Leu Ala Val Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Arg Asn
      770                    775                    780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785                    790                    795                    800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
                  805                    810                    815
Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
              820                    825                    830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
          835                    840                    845
Leu Glu Phe Arg Gly Glu Ser Ile Ile Val Ser Leu Ile Leu Arg Asn
      850                    855                    860
Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu
865                    870                    875                    880
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
                  885                    890                    895
Gln Arg Phe Phe Glu Ile Lys Lys Glu Asn Glu Val Val Asp Leu Trp
          900                    905                    910
Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
      915                    920                    925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
      930                    935                    940
His Val Asp Ile Leu Leu Arg Ile Ser Ala Asn Ile Arg Asn Glu Ala
945                    950                    955                    960
Lys Ile Ser Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
              965                    970                    975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
          980                    985                    990
Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
      995                    1000                   1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Ser Asp Ser Ala Ile His
      1010                   1015                   1020
Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
1025                   1030                   1035                   1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
              1045                   1050                   1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
          1060                   1065                   1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
      1075                   1080                   1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
      1090                   1095                   1100
Leu Ser Val Val Val Asp Ser Ile Glu Ile Pro Thr Lys Ser Asn Gly
```

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```
1105                1110                    1115                    1120
Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Thr Ser Trp
             1125                    1130                    1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys
             1140                    1145                    1150
Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
             1155                    1160                    1165
Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys
       1170                    1175                    1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185                    1190                    1195                    1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Arg Glu Gln Leu Glu Ala
1205                    1210                    1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
             1220                    1225                    1230
Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys
             1235                    1240                    1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
       1250                    1255                    1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265                    1270                    1275                    1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
             1285                    1290                    1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
       1300                    1305                    1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
       1315                    1320                    1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
       1330                    1335                    1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
1345                    1350                    1355                    1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
             1365                    1370                    1375
Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
       1380                    1385                    1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
       1395                    1400                    1405
Asn Leu Ile Glu Ser Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
       1410                    1415                    1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp
1425                    1430                    1435                    1440
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
             1445                    1450                    1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
       1460                    1465                    1470
Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu
       1475                    1480                    1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
       1490                    1495                    1500
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
1505                    1510                    1515                    1520
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
             1525                    1530                    1535
Arg Ser Ala Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly
       1540                    1545                    1550
Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
       1555                    1560                    1565
Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
       1570                    1575                    1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Asp
1585                    1590                    1595                    1600
Leu Leu Thr Pro Ile Pro Ser Pro Met Val Asn Leu Thr Gln Val Ile
```

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```
                    1605                   1610                   1615
Asp Pro Thr Glu Gln Leu Ala Tyr Phe Pro Lys Ile Thr Phe Glu Arg
            1620                   1625                   1630
Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr
        1635                   1640                   1645
Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
    1650                   1655                   1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
1665                   1670                   1675                   1680
Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
                1685                   1690                   1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
            1700                   1705                   1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
        1715                   1720                   1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp
    1730                   1735                   1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
1745                   1750                   1755                   1760
His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr
                1765                   1770                   1775
Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val
            1780                   1785                   1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr
        1795                   1800                   1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn
    1810                   1815                   1820
Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
1825                   1830                   1835                   1840
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
                1845                   1850                   1855
His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
            1860                   1865                   1870
Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn
        1875                   1880                   1885
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
    1890                   1895                   1900
Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Arg Arg Leu Leu Thr Leu
1905                   1910                   1915                   1920
Gln Ser Asn His Ser Ser Val Ala Thr Val Gly Gly Ser Lys Val Ile
                1925                   1930                   1935
Glu Ser Lys Trp Leu Thr Asn Lys Ala Asn Thr Ile Ile Asp Trp Leu
            1940                   1945                   1950
Glu His Ile Glu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
        1955                   1960                   1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
    1970                   1975                   1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985                   1990                   1995                   2000
Leu Val Ser Lys Lys
                2005
```

```
<210> 331
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 331
Met Asp Pro Leu Asn Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1               5                   10                  15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
```

```
                20                    25                    30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
        35                    40                    45
Ala Ile Glu Asn Pro Val Ile Glu His Val Arg Leu Lys Asn Ala Val
50                    55                    60
Asn Ser Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
65                    70                    75                    80
Met Gln His Glu Ile Met Lys Asn Val His Ser Cys Glu Leu Thr Leu
                85                    90                    95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Thr Leu Lys Leu
            100                   105                   110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asp Thr
            115                   120                   125
Ser Ile Leu Ser Phe Ile Asp Val Glu Phe Leu Ser Ser Trp Val Ser
            130                   135                   140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145                   150                   155                   160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
                165                   170                   175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Ile Val Lys Ser
            180                   185                   190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
            195                   200                   205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
210                   215                   220
Val Ser Asn Ser Leu Asn Glu Asn Gln Glu Gly Leu Gly Leu Arg Ser
225                   230                   235                   240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
                245                   250                   255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
            260                   265                   270
Glu Gly Phe Ile Met Ser Glu Leu Ile Leu Arg Ile Thr Glu His Ala Gln
        275                   280                   285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Asp Gln
290                   295                   300
Leu Thr Lys Leu Lys Asn Lys Asn Arg Leu Arg Val His Gly Thr Val
305                   310                   315                   320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
                325                   330                   335
Gly Asp Thr Leu Arg Cys Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
            340                   345                   350
Asn Ala Ala Gln Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
            355                   360                   365
Val Asp Glu Arg Asp Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
370                   375                   380
Thr Lys Ile Leu Arg Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385                   390                   395                   400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
                405                   410                   415
Lys Ile Lys Asn Leu Ile Val Leu Ser Lys Arg Trp Thr Met Tyr Phe
            420                   425                   430
Lys Ala Lys Asn Tyr Pro Ser Gln Leu Glu Leu Ser Glu Gln Asp Phe
            435                   440                   445
Leu Glu Leu Ala Ala Ile Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
450                   455                   460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465                   470                   475                   480
Lys Arg Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr
                485                   490                   495
Ile Lys Asn Arg Tyr Leu Glu Glu Thr Phe Asn Ala Ser Asp Ser Leu
            500                   505                   510
Lys Thr Arg Arg Val Leu Glu Tyr Tyr Leu Lys Asp Asn Lys Phe Asp
```

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```
          515                    520                    525
Gln Lys Glu Leu Lys Ser Tyr Val Val Arg Gln Glu Tyr Leu Asn Asp
     530                    535                    540
Lys Glu His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
545                    550                    555                    560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
               565                    570                    575
Leu Ala Glu Lys Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
               580                    585                    590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
          595                    600                    605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Arg Asn Asp Ser Tyr Asn
     610                    615                    620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
625                    630                    635                    640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
               645                    650                    655
Glu Leu His Gly Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
               660                    665                    670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
          675                    680                    685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr
     690                    695                    700
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
705                    710                    715                    720
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
               725                    730                    735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
               740                    745                    750
Lys Pro Val Lys Leu Ser Glu Gly Leu Asp Glu Val Lys Ala Asp Tyr
          755                    760                    765
Arg Leu Ala Ile Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Arg Asn
     770                    775                    780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785                    790                    795                    800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
               805                    810                    815
Pro Ile Lys Lys Val Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
               820                    825                    830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Leu Glu
          835                    840                    845
Leu Glu Phe Arg Gly Glu Ser Ile Ile Ile Val Ser Leu Ile Leu Arg Asn
     850                    855                    860
Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu
865                    870                    875                    880
Ala Gly Lys Gln Leu Phe Lys Gly Leu Asn Lys Thr Leu Thr Ser Val
               885                    890                    895
Gln Arg Phe Phe Glu Ile Lys Lys Glu Asn Glu Val Val Asp Leu Trp
          900                    905                    910
Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
     915                    920                    925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
930                    935                    940
His Val Asp Ile Leu Leu Lys Ile Ser Ala Asn Ile Lys Asn Glu Thr
945                    950                    955                    960
Lys Val Ser Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
               965                    970                    975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
          980                    985                    990
Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
     995                    1000                   1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Ser Asp Ser Ala Ile His
```

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      1010                    1015                    1020
Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Glu Asn Ile Thr
1025                    1030                    1035                    1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
                  1045                    1050                    1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
                  1060                    1065                    1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
            1075                    1080                    1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
      1090                    1095                    1100
Leu Ser Val Val Val Asp Ser Leu Gly Ile Glu Pro Ile Lys Ser Asn Gly
1105                    1110                    1115                    1120
Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Glu Thr Ser Trp
                  1125                    1130                    1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys
                  1140                    1145                    1150
Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
            1155                    1160                    1165
Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys
      1170                    1175                    1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185                    1190                    1195                    1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Arg Glu Gln Leu Glu Ala
                  1205                    1210                    1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
            1220                    1225                    1230
Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys
            1235                    1240                    1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
      1250                    1255                    1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265                    1270                    1275                    1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
                  1285                    1290                    1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
            1300                    1305                    1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
      1315                    1320                    1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
      1330                    1335                    1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
1345                    1350                    1355                    1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
                  1365                    1370                    1375
Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
            1380                    1385                    1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
      1395                    1400                    1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
      1410                    1415                    1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp
1425                    1430                    1435                    1440
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
                  1445                    1450                    1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
            1460                    1465                    1470
Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu
      1475                    1480                    1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
      1490                    1495                    1500
Glu Pro Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
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      1505              1510                1515                1520
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
          1525              1530                1535
Arg Ser Ala Glu Leu His Glu Ile Pro Trp Ile Val Asn Ala Glu Gly
          1540              1545                1550
Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
      1555              1560                1565
Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
      1570              1575                1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
1585              1590                1595                1600
Leu Leu Thr Pro Ile Ser Ser Pro Met Val Asn Leu Thr Gln Val Ile
              1605              1610                1615
Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Lys Ile Thr Phe Glu Arg
          1620              1625                1630
Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr
      1635              1640                1645
Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
      1650              1655                1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
1665              1670                1675                1680
Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
          1685              1690                1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
          1700              1705                1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
      1715              1720                1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp
      1730              1735                1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
1745              1750                1755                1760
His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr
              1765              1770                1775
Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val
          1780              1785                1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr
      1795              1800                1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn
      1810              1815                1820
Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
1825              1830                1835                1840
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
              1845              1850                1855
His His Asn Ser Leu Pro Cys His Gly Glu Ile Glu Gln Asn Ser Lys Met
          1860              1865                1870
Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn
      1875              1880                1885
Lys Ser Ile Glu Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
      1890              1895                1900
Pro Ile Asn Lys Lys Glu Leu Asp Arg Gln Arg Arg Leu Leu Thr Leu
1905              1910                1915                1920
Gln Ser Asn His Ser Ser Val Ala Thr Val Gly Gly Ser Lys Ile Ile
              1925              1930                1935
Glu Ser Lys Trp Leu Thr Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
          1940              1945                1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
      1955              1960                1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
      1970              1975                1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985              1990                1995                2000
Leu Val Ser Lys Lys
```

152

2005

```
<210> 332
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 332
Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1               5                   10                  15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
            20                  25                  30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
        35                  40                  45
Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
    50                  55                  60
Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
65                  70                  75                  80
Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
                85                  90                  95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
            100                 105                 110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
        115                 120                 125
Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
    130                 135                 140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145                 150                 155                 160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
                165                 170                 175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
            180                 185                 190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
        195                 200                 205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
    210                 215                 220
Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Leu Arg Ser
225                 230                 235                 240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
                245                 250                 255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
            260                 265                 270
Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
        275                 280                 285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
    290                 295                 300
Leu Ser Val Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
305                 310                 315                 320
Leu Glu Asn Asn Asn Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
                325                 330                 335
Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
            340                 345                 350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
        355                 360                 365
Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
    370                 375                 380
Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385                 390                 395                 400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
                405                 410                 415
Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Ala Met Tyr Phe
```

153

```
                420                      425                      430
Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
            435                      440                      445
Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
        450                      455                      460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465                      470                      475                      480
Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr
                485                      490                      495
Ile Lys Asn Gln Tyr Leu Glu Glu Ala Phe Asn Ala Ser Asp Ser Gln
            500                      505                      510
Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
        515                      520                      525
Gln Lys Glu Leu Lys Arg Tyr Val Ile Lys Gln Glu Tyr Leu Asn Asp
        530                      535                      540
Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Gly Leu Ser Val
545                      550                      555                      560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
                565                      570                      575
Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
            580                      585                      590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
        595                      600                      605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
        610                      615                      620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
625                      630                      635                      640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
                645                      650                      655
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
            660                      665                      670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
        675                      680                      685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Gln Glu Gln Ser Gly Leu Tyr
        690                      695                      700
Arg Tyr His Met Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
705                      710                      715                      720
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
                725                      730                      735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
            740                      745                      750
Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
        755                      760                      765
Ser Leu Ala Ile Arg Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
        770                      775                      780
Ile Gly His Lys Leu Lys Gly Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785                      790                      795                      800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
                805                      810                      815
Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
            820                      825                      830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
        835                      840                      845
Leu Glu Phe Arg Gly Glu Ser Ile Leu Val Ser Leu Ile Leu Arg Asn
        850                      855                      860
Phe Trp Leu Tyr Asn Leu Tyr Met Tyr Glu Ser Lys Gln His Pro Leu
865                      870                      875                      880
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
                885                      890                      895
Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
            900                      905                      910
Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
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154

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            915                 920                 925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
    930                 935                 940
His Val Asp Leu Leu Leu Lys Val Ser Asn Asn Ile Lys Asp Glu Thr
    945                 950                 955                 960
Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Gln Arg
            965                 970                 975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
        980                 985                 990
Arg Gln Ala Lys Val Thr Ser Ala Ile Asn Arg Thr Ala Val Thr Ser
        995                 1000                1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Cys Asp Ser Ala Ile His
    1010                1015                1020
Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
1025                1030                1035                1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
                1045                1050                1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
        1060                1065                1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
    1075                1080                1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
    1090                1095                1100
Leu Ser Val Ile Ile Asn Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
1105                1110                1115                1120
Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
                1125                1130                1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Val Thr Cys
        1140                1145                1150
Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
    1155                1160                1165
Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
    1170                1175                1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185                1190                1195                1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
                1205                1210                1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
        1220                1225                1230
Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
    1235                1240                1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Ala
    1250                1255                1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265                1270                1275                1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
                1285                1290                1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
        1300                1305                1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
    1315                1320                1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
    1330                1335                1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
1345                1350                1355                1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
                1365                1370                1375
Asp Ile Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
        1380                1385                1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
    1395                1400                1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
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155

```
        1410              1415                   1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Arg Lys Asp Trp
1425              1430              1435                   1440
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Val Phe
        1445              1450                   1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
        1460              1465              1470
Lys Asn Val Lys Asp Glu Asp Ile Ile Asp Glu Ser Ile Asp Lys Leu
        1475              1480              1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
        1490              1495              1500
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
1505              1510              1515                   1520
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
        1525              1530                   1535
Arg Val Val Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly
        1540              1545              1550
Glu Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
        1555              1560              1565
Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
1570              1575              1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
1585              1590              1595                   1600
Leu Phe Asn Pro Ser Ser Ser Pro Met Phe Asn Leu Thr Gln Val Ile
        1605              1610                   1615
Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Arg Ile Ile Phe Glu Arg
        1620              1625                   1630
Leu Lys Ser Tyr Asp Thr Ser Ser Asp Tyr Asn Lys Gly Lys Leu Thr
        1635              1640              1645
Arg Asn Tyr Met Thr Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
        1650              1655              1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
1665              1670              1675                   1680
Gly Lys Leu Ile Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
        1685              1690                   1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
        1700              1705                   1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
        1715              1720              1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Asp Leu Asn Arg Val Ile Asp
        1730              1735              1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
1745              1750              1755                   1760
His Trp Asp Leu Ile His Arg Ile Ser Lys Asp Ala Leu Leu Ile Thr
        1765              1770              1775
Leu Cys Asp Ala Glu Phe Lys Asn Arg Asp Asp Phe Phe Lys Met Val
        1780              1785              1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Ala Tyr
        1795              1800              1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Val Asp Cys Asn
        1810              1815              1820
Ile Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
1825              1830              1835                   1840
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
        1845              1850                   1855
His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
        1860              1865              1870
Arg Ile Ala Val Cys Asn Asp Phe Tyr Ala Ser Lys Lys Leu Asp Asn
        1875              1880              1885
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
        1890              1895              1900
Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Lys Lys Leu Leu Thr Leu
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156

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1905                    1910                    1915                    1920
Gln Ser Asn His Ser Ser Ile Ala Thr Val Gly Gly Ser Lys Ile Ile
            1925                    1930                    1935
Glu Ser Lys Trp Leu Lys Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
            1940                    1945                    1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
            1955                    1960                    1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
    1970                    1975                    1980
Leu Gly Asn Ala Glu Ile Glu Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985                    1990                    1995                    2000
Leu Val Ser Lys Lys
                2005


<210> 333
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 333
Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1                   5                   10                  15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
            20                  25                  30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Lys Asp Asn Thr Ala Lys Val
        35                  40                  45
Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
    50                  55                  60
Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Ile Asn
65                  70                  75                  80
Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
                85                  90                  95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
            100                 105                 110
Ser Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
        115                 120                 125
Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
    130                 135                 140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145                 150                 155                 160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
                165                 170                 175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
            180                 185                 190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
        195                 200                 205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
    210                 215                 220
Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Phe Arg Ser
225                 230                 235                 240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
                245                 250                 255
Met Leu Ser Leu Cys Ser Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
            260                 265                 270
Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
    275                 280                 285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
    290                 295                 300
Leu Ser Met Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
305                 310                 315                 320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
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                    325                    330                    335
Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
            340                    345                    350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
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Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
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Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
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Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
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Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Val Met Tyr Phe
            420                    425                    430
Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
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Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
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Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465                    470                    475                    480
Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Ile
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Ile Lys Asn Gln Tyr Leu Glu Glu Val Phe Asn Ala Ser Asp Ser Gln
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Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
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Gln Lys Asp Leu Lys Arg Tyr Val Leu Lys Gln Glu Tyr Leu Asn Asp
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Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
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Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
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Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
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Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Met
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Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
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Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
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Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
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Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
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Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr
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Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
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Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
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Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
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Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
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Ser Leu Ala Ile Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
            770                    775                    780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785                    790                    795                    800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
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Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
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Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu
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Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
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Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
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Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
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Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
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His Val Asp Leu Leu Lys Lys Val Ser Asn Asn Ile Lys Asn Glu Thr
945                    950                    955                    960
Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
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Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
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Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
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His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
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Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
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Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
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Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
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Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
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Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
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Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
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Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
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Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
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Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
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Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
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Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
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Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
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Asp Ile Leu Thr Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
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Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
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Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
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Ile Leu Thr Glu Gln Cys Val Glu Asn Asn Ile Phe Arg Lys Asp Trp
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Lys Asn Val Lys Asp Glu Asp Ile Ile Glu Asp Glu Ser Ile Asp Lys Leu
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Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
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His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
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His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
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Arg Ile Ala Val Cys Asn Asp Phe His Ala Ser Lys Lys Leu Asp Asn
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Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
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Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Lys Lys Leu Leu Thr Leu
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Gln Ser Asn His Ser Ser Ile Ala Thr Val Gly Gly Ser Lys Ile Ile
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Glu Ser Lys Trp Leu Lys Asn Lys Ala Ser Thr Ile Ile Ile Asp Trp Leu
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Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
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Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
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162

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agagaaaact atttccatgg aaataaattta attgaatctt tatctgcagc acttgcatgc 4260
```

```
cactggtgtg gaatattaac agaacagtgt gtagaaaaca atatctttag gaaagactgg 4320
ggtgatgggt tcatatcaga tcatgccttc atggatttca agatatttct atgtgtattt 4380
aaaaccaaac ttttatgtag ttggggatcc caagggaaaa atgtaaaaga tgaagataaa 4440
atagatgaat ccattgacaa attattaaga attgacaaca cttttggag aatgttcagc 4500
aaagtcatgt ttgaatcaaa ggtcaaaaaa agaataatgt tatatgtgt caaattccta 4560
tcattagtag gttatatagg atttaaaact tggtttatag agcagttaag agtagtagaa 4620
ttgtcatggga tgcctggat tgtcaatgct gaagggggac tagttgaaat taaaccaatc 4680
aaaatttatt tgcagttaat agaacaaagt ctatctttaa gaataactgt ttttgaattat 4740
acagacatgg cacatgctct tacacgatta attaggaaga aattgatgtg tgataatgca 4800
ctcttcaatc caagttcatc accaatgttt agtctaactc aagttatcga tcctacaaca 4860
cagctagact attttcctaa ggtgatattt gaaaggttaa aaagttatga taccagttca 4920
gactacaaca aaggaagtt aacaagaaat tactgacat tattaccatg gcagcacgta 4980
aacaggtata attttgtctt tagttcaaca ggatgtaaaa tcagcttgaa gacatgcatc 5040
gggaaattga taaaggactt aaacctaag gttctttact ttattggaga aggagcaggt 5100
aactggatgg caagaacagc atgtgagtat cctgacataa aatttgtata taggagtta 5160
aaggatgatc ttgatcatca ttacccatta gaatatcaaa gggtaatagg tgatttaaat 5220
agggtaatag atggtggtga aggactatca atggagacca cagatgcaac tcaaaagact 5280
cattgggact taatacacag aataagtaaa gatgctttat tgataacatt gtgtgatgca 5340
gaattcaaaa acagagatga tttctttaaa atggtaattc tttggagaaa acatgtatta 5400
acggactgca atataaaatt accatttttt gtaaggtctg tagctactttt tattatgcaa 5460
ggagacaaat tgtcaggatc aggatgttac atactttaa cattaggtca tcacaataat 5520
ctgccatgcc atggagaaat acaaaattcc aaatgagaa tagcagtgtg taatgattgt 5580
catgcctcaa aaaactaga caacaaatca attgaagcta actgtaaatc tcttctatca 5640
ggattaagaa taccaataaa caaaaaagag ttaaatagac aaaagaaact gttaacacta 5700
caaagcaatc attcttccat agcaacagtt ggcggcagta agattataga atccaaatgg 5760
ttaaagaata aagcaagtac aataattgat tggttagagc atatcttgaa ttctccaaaa 5820
ggtgaattaa acatatgattt cttttgaagca ttagagaaca cataccccaa tatgatcaag 5940
cttatagata acctgggaaa tgcagagata aaaaaactaa tcaaagttcc tgggtatatg 6000
cttgtgagta agaagtaa                                                 6018
```

```
<210> 338
<211> 187
<212> PRT
<213> human metapneumo virus

<400> 338
Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
1               5                   10                  15
Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
            20                  25                  30
Arg Tyr Leu Leu Ile Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
        35                  40                  45
Asn Thr Asp Arg Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
    50                  55                  60
Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
65                  70                  75                  80
Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
                85                  90                  95
Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Val Glu Val Arg Gln
            100                 105                 110
Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
        115                 120                 125
Leu Val Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
    130                 135                 140
Asn Asn Leu Lys Arg Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
145                 150                 155                 160
Leu Ile Ile Asp Ser Asp Ser Ala Gly Ala Asp Asn Asp Ser Ser Tyr Ala
                165                 170                 175
Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
```

168

```
                    180                    185


<210> 339
<211> 187
<212> PRT
<213> human metapneumo virus

<400> 339
Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1               5                   10                  15
Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
            20                  25                  30
Arg Tyr Leu Leu Ile Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
        35                  40                  45
Asn Thr Asp Arg Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
    50                  55                  60
Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
65                  70                  75                  80
Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
                85                  90                  95
Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Val Glu Val Arg Gln
            100                 105                 110
Ala Arg Asp Ser Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
        115                 120                 125
Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
        130                 135                 140
Asn Asn Leu Lys Arg Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
145                 150                 155                 160
Leu Ile Ile Asp Leu Ser Ala Gly Ala Asp Asn Asp Ser Ser Tyr Ala
                165                 170                 175
Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
            180                 185


<210> 340
<211> 187
<212> PRT
<213> human metapneumo virus

<400> 340
Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1               5                   10                  15
Arg Gly Ser Asp Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
            20                  25                  30
Arg Tyr Leu Leu Leu Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
        35                  40                  45
Asn Thr Asp Lys Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
    50                  55                  60
Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
65                  70                  75                  80
Gly Tyr Ile Asp Asp Asn Gln Gly Ile Thr Lys Ala Ala Ala Cys Tyr
                85                  90                  95
Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Thr Glu Val Arg Gln
            100                 105                 110
Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
        115                 120                 125
Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
        130                 135                 140
Asn Asn Leu Lys Lys Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
145                 150                 155                 160
Leu Ile Ile Asp Leu Ser Ala Gly Thr Asp Asn Asp Ser Ser Tyr Ala
```

```
                           165                 170                 175
Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
                  180                 185


<210> 341
<211> 187
<212> PRT
<213> human metapneumo virus

<400> 341
Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1               5                  10                  15
Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
                 20                  25                  30
Arg Tyr Leu Leu Leu Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
        35                  40                  45
Asn Thr Asp Lys Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
 50                  55                  60
Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
65                  70                  75                  80
Gly Tyr Ile Asp Asn Asn Gln Gly Ile Thr Lys Ala Ala Ala Cys Tyr
                 85                  90                  95
Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Ile Glu Val Arg Gln
             100                 105                 110
Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
         115                 120                 125
Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
     130                 135                 140
Asn Asn Leu Lys Lys Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
 145                 150                 155                 160
Leu Ile Ile Asp Leu Ser Ala Gly Thr Asp Asn Asp Ser Ser Tyr Ala
                 165                 170                 175
Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
                 180                 185


<210> 342
<211> 564
<212> DNA
<213> human metapneumo virus

<400> 342
atgtctcgca aggctccgtg caaatatgaa gtgcggggca aatgcaatag aggaagtgag 60
tgcaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaat 120
tatttattaa atcaactttt aaggaacact gatagagctg atggcttatc aataatatca 180
ggagcaggca gagaagatag gacacaagat tttgtcctag gttccaccaa tgtggttcaa 240
ggttatatcg atgataacca aagcataaca aaagctgcag cctgttacag tctacataat 300
atatcaaac aactacaaga agttgaagtt aggcaggcta gagataacaa actatctgac 360
agcaaacatg tagcacttca caacttagtc ctatcttata tggagatgag caaaactcct 420
gcatctttaa tcaacaatct caagagactg ccgagagaga aactgaaaaa attagcaaag 480
ctcataattg acttatcagc aggtgctgaa aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtga                                        564


<210> 343
<211> 564
<212> DNA
<213> human metapneumo virus

<400> 343
atgtctcgca aggctccatg caaatatgaa gtgcggggca aatgcaacag aggaagtgag 60
tgtaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120
```

```
tatctattaa atcagctttt aaggaacact gatagagctg atggcctatc aataatatca 180
ggcgcaggca gagaagacag aacgcaagat tttgttctag gttccaccaa tgttggttcaa 240
ggttatattg atgataacca aagcataaca aaagctgcag cctgctacag tctacacaac 300
ataatcaagc aactacaaga agttgaagtt aggcaggcta gagatagcaa actatctgac 360
agcaagcatg tggcactcca taacttaatc ttatcttaca tggagatgag caaaactccc 420
gcatctttaa tcaacaatct taaaagactg ccgagagaaa aactgaaaaa attagcaaag 480
ctgataattg acttatcagc aggcgctgac aatgactctt catatgccct gcaagacagt 540
gaaagcacta atcaagtgca gtga                                         564
```

```
<210> 344
<211> 564
<212> DNA
<213> human metapneumo virus
```

```
<400> 344
atgtctcgta aggctccagt caaatatgaa gtgcggggca aatgcaacag agggagtgat 60
tgcaaattca atcacaatta ctggagttgg cctgatagat atttattgtt aagatcaaat 120
ggagcaggta gagaagatag aactcaagac tttgttcttg gttctactaa tgtggttcaa 180
gggtacattg atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgat 360
agcaaacatg tggcgctcca caacttgata ttatctctata tggagatgag caaaactcct 420
gcatctctaa tcaacaacct aaagaaacta ccaagggaaa aactgaagaa attagcaaga 480
ttaataattg atttatcagc aggaactgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtaa                                         564
```

```
<210> 345
<211> 564
<212> DNA
<213> human metapneumo virus
```

```
<400> 345
atgtctcgca aagctccatg caaatatgaa gtacggggca agtgcaacag gggaagtgag 60
tgcaaattca accacaatta ctggagctgg cctgatagat atttattgtt aagatcaaat 120
tatctcttga atcagcttt aagaaacact gataaggctg atgtttgtc aataatatca 180
ggagcaggta gagaagatag gactcaagac tttgttcttg gttctactaa tgtggttcaa 240
gggtacattg ataacaatca aggaataaca aaggctgcag cttgctatag tctacataac 300
ataataaaac agctacaaga aatagaagta agacaggcta gagataataa gctttctgat 360
agcaaacatg tggcacttca caacttgata ttatctctata tggagatgag caaaactcct 420
gcatccctga ttaataacct aaagaaacta ccaagagaaa aactgaagaa attagcgaaa 480
ttaataattg atttatcagc aggaactgat aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtaa                                         564
```

```
<210> 346
<211> 71
<212> PRT
<213> human metapneumo virus
```

```
<400> 346
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1               5                   10                  15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Asp Met Ile
            20                  25                  30
Trp Thr His Lys Asp Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
        35                  40                  45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
    50                  55                  60
Tyr Val Lys Ala Tyr Leu Ser
65                  70
```

```
<210> 347
```

171

```
<211> 71
<212> PRT
<213> human metapneumo virus

<400> 347
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1               5                   10                  15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Glu Met Ile
            20                  25                  30
Trp Thr Gln Lys Glu Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
        35                  40                  45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
    50                  55                  60
Tyr Val Lys Ala Tyr Leu Ser
65                  70


<210> 348
<211> 71
<212> PRT
<213> human metapneumo virus

<400> 348
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1               5                   10                  15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
            20                  25                  30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys
        35                  40                  45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile
    50                  55                  60
Tyr Val Lys Thr Tyr Leu Ser
65                  70


<210> 349
<211> 71
<212> PRT
<213> human metapneumo virus

<400> 349
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1               5                   10                  15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
            20                  25                  30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys
        35                  40                  45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile
    50                  55                  60
Tyr Val Lys Ala Tyr Leu Ser
65                  70


<210> 350
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 350
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag tgagcatggt   60
ccagtttca ttactataga ggttgatgac atgatatgga ctcacaagga cttaaaagaa   120
gctttatctg atgggatagt gaagtctcat actaacattt acaattgtta tttagaaaac   180
```

```
atagaaatta tatatgtcaa ggcttactta agttag                              216

<210> 351
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 351
atgactcttc atatgccctg caagacagtg aaagcactaa tcaagtgcag tgagcatggt   60
cctgttttca ttactataga ggttgatgaa atgatatgga ctcaaaaaga attaaaagaa  120
gctttgtccg atgggatagt gaagtctcac accaacattt acaattggta tttagaaaac  180
atagaaatta tatatgtcaa ggcttactta agttag                              216

<210> 352
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 352
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag taaacatggt   60
cccaaattca ttaccataga ggcgatgat atgatatgga ctcacaaaga attaaaagaa  120
acactgtctg atgggatagt aaaatcacac accaatattt atagttgtta cttagaaaat  180
atagaaataa tatatgttaa aacttactta agttag                              216

<210> 353
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 353
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag taagcatggt   60
cccaaattca ttaccataga ggcagatgat atgatatgga cacacaaaga attaaaggag  120
acactgtctg atgggatagt aaaatcacac accaatattt acagttgtta tttagaaaat  180
atagaaataa tatatgttaa agcttactta agttag                              216

<210> 354
<211> 727
<212> DNA
<213> human metapneumo virus

<400> 354
atgtctcgca aggctccgtg caaatatgaa gtgcggggca aatgcaatag aggaagtgag   60
tgcaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaat  120
tatttattaa atcaacttt aaggaacact gatagagctg atggcttatc aataatcatca  180
ggagcaggca gagaagatag gacacaagat tttgtcctag gttccaccaa tgtggttcaa  240
ggtctatttg atgataacca aagcataaca aaagctgcag cctgttacag tctacataat  300
ataatcaaac aactacaaga agttgaagtt aggcaggcta gagataacaa actatctgac  360
agcaaacatg tagcaacttca caacttagtc ctatcttata tggagatgag caaaactcct  420
gcatcttttaa tcaacaatct caagagactg ccgagagaga aactgaaaaa attagcaaag  480
ctcataattg acttatcagc aggtgctgaa aatgactctt catatgcctt gcaagacagt  540
gaaagcacta atcaagtgca gtgagcagtg tccagttttc attactatag aggttgatga  600
catgatatgg actcacaagg acttaaaaga agcttttatct gatgggatag tgaagtctca  660
tactaacatt tacaattgtt atttagaaaa catagaaatt atatatgtca aggcttactt  720
aagttag                                                              727

<210> 355
<211> 727
<212> DNA
<213> human metapneumo virus

<400> 355
atgtctcgca aggctccatg caaatatgaa gtgcggggca aatgcaacag aggaagtgag   60
```
173

```
tgtaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120
tatctattaa atcagctttt aaggaacact gatagagctg atggcctatc aataatatca 180
ggcgcaggca gagaagacag aacgcaagat tttgttctag gttccaccaa tgtcggttcaa 240
ggttatattg atgataacca aagcataaca aaagctgcag cctgctacag tctacacaac 300
ataatcaagc aactacaaga agttgaagtt agcgcaggcta gagatgcaa actatctgac 360
agcaagcatg tggcactcca taacttaatc ttatcttaca tggagatgag caaaactcct 420
gcatctttaa tcaacaatct taaagactg ccgagagaaa aactgaaaaa attagcaaag 480
cgataattg acttatcagc aggcgctgac aatgactctt catatgccct gcaagacagt 540
gaaagcacta atcaagtgca gtgagcatgg tcctgttttc attactatag aggttgatga 600
aatgatatgg actcaaaaag aattaaaaga agctttgtcc gatgggatag tgaagtccaa 660
caccaacatt tacaattgtt atttagaaaa catagaaatt atatatgtca aggcttactt 720
aagttag                                                         727
```

```
<210> 356
<211> 727
<212> DNA
<213> human metapneumo virus
```

```
<400> 356
atgtctcgta aggtccatga caaatatgaa gtgcggggca aatgcaacag agggagtgat 60
tgcaaattca atcacaatta ctggagttgg cctgatagat atttattgtt aagatcaaat 120
tatctcttaa atcagctttt aagaaacaca gataaggctg atggttgtc aataatatca 180
ggagcaggta gagaagatag aactcaagac tttgttcttg gttctactaa tgtcggttca 240
gggtacattg atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgac 360
agcaaacatg tggcgctcca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatctctaa tcaacaacct aaagaaactc ccaagggaaa aactgaagaa attagcaaga 480
ttaataattg atttatcagc aggactgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtaaacatgg tcccaaattc attaccatag aggcagatga 600
tatgatatgg actcacaaag aattaaaaga aacactgtct gatgggatag taaaatcaca 660
caccaatatt tatagttgtt acttagaaaa tatagaaata atatatgtta aaacttactt 720
aagttag                                                         727
```

```
<210> 357
<211> 727
<212> DNA
<213> human metapneumo virus
```

```
<400> 357
atgtctcgca aagtccatg caaatatgaa gtacgcgggca agtgcaacag gggaagtgag 60
tgcaaattca accacaatta ctggagctgg cctgataggt atttattgtt aagatcaaat 120
tatctcttga atcagctttt aagaaacact gataaggctg atggtttgtc aataatatca 180
ggagcaggta gagaagatag gactcaagac tttgttcttg gttctactaa tgtcggttca 240
gggtacattg ataacaatca aggaataaca aaggctgcag cttgctatag tctacacaac 300
ataataaaac agctacaaga aataagagta agacaggcta gagataataa gctttctgac 360
agcaaacatg tggcacttca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatccctga ttaataacct aaagaaacta ccaaggaaa aactgaagaa attagcaaga 480
ttaataattg atttatcagc aggaactgat aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtaagcatgg tcccaaattc attaccatag aggcagatga 600
tatgatatgg acacacaaag aattaaagga gacactgtct gatgggatag taaaatcaca 660
caccaatatt tacagttgtt atttagaaaa tatagaaata atatatgtta aagcttactt 720
aagttag                                                         727
```

```
<210> 358
<211> 254
<212> PRT
<213> human metapneumo virus
```

```
<400> 358
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1               5                   10                  15
Ala Val Gln Val Asp Leu Ile Glu Lys Asp Leu Leu Pro Ala Ser Leu
```

```
                    20                        25                        30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
        35                        40                        45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
    50                        55                        60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65                        70                        75                        80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
                    85                        90                        95
Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val
                100                       105                       110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
            115                       120                       125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
    130                       135                       140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile
145                       150                       155                       160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
                165                       170                       175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
            180                       185                       190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
        195                       200                       205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
    210                       215                       220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys
225                       230                       235                       240
Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
                245                       250
```

```
<210> 359
<211> 254
<212> PRT
<213> human metapneumo virus

<400> 359
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1                   5                        10                       15
Ala Val Gln Val Asp Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
                    20                        25                        30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
        35                        40                        45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
    50                        55                        60
Gln Ser Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65                        70                        75                        80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
                    85                        90                        95
Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val
                100                       105                       110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
            115                       120                       125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
    130                       135                       140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile
145                       150                       155                       160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
                165                       170                       175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
            180                       185                       190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
```

```
            195                      200                      205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
    210                      215                      220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys
225                      230                      235                  240
Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Ser
            245                      250
```

```
<210> 360
<211> 254
<212> PRT
<213> human metapneumo virus

<400> 360
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1               5                       10                      15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
            20                      25                      30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
            35                      40                      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
    50                      55                      60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65                      70                      75                  80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
            85                      90                      95
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val
            100                     105                     110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
    115                     120                     125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
    130                     135                     140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Ile Pro Val Thr Ile
145                     150                     155                 160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
            165                     170                     175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
            180                     185                     190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
    195                     200                     205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
    210                     215                     220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys
225                     230                     235                 240
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
            245                     250
```

```
<210> 361
<211> 254
<212> PRT
<213> human metapneumo virus

<400> 361
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1               5                       10                      15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
            20                      25                      30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
            35                      40                      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
```

```
     50                        55                      60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65                        70                      75                      80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
                  85                      90                      95
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val
                  100                     105                     110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
            115                     120                     125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
      130                     135                     140
Ala Leu Cys Asp Phe Met Glu Leu Glu Lys Asn Ile Pro Val Thr Ile
145                     150                     155                     160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
                  165                     170                     175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
            180                     185                     190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
      195                     200                     205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
210                     215                     220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys
225                     230                     235                     240
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
                  245                     250
```

```
<210> 362
<211> 765
<212> DNA
<213> human metapneumo virus

<400> 362
atggagtcct acctagtaga cacttatcaa ggcattcctt acacagcagc tgttcaagtt   60
gatctaatag aaaaggacct gttacctgca agcctaacaa tatggttccc tttgtttcag  120
gccaacacac caccagcagt gctgctcgat cagctaaaaa ccctgacaat aaccactctg  180
tatgctgcat cacaaaatgg tccaatactc aaagtgaatg catcagccca aggtgcagca  240
atgtctgtac ttcccaaaaa atttgaagtc aatgcgactg tagcactcga tgaatatagc  300
aaactggaat ttgacaaact cacagtctgt gaagtaaaaa cagtttactt aacaaccatg  360
aaaccatacg ggatggtatc aaaatttgtg agctcagcca aatcagttgg caaaaaaaca  420
catgatctaa tcgcactatg tgattttatg gatctagaaa agaacacacc tgttacaata  480
ccagcattca tcaaatcagt ttcaatcaaa gagagtgagt cagctactgt tgaagctgct  540
ataagcagtg aagcagacca agctctaaca caggccaaaa ttgcacctta tgcgggatta  600
attatgatca tgactatgaa caatcccaaa ggcatattca aaaagcttgg agctgggact  660
caagtccatg tagaactagg agcatatgtc caggctgaaa gcataagcaa aatatgcaag  720
acttggagcc atcaagggac aagatatgtc ttgaagtcca gataa                  765

<210> 363
<211> 765
<212> DNA
<213> human metapneumo virus

<400> 363
atggagtcct atctggtaga cacttatcaa ggcatccctt acacagcagc tgttcaagtt   60
gatctagtag aaaaggacct gttacctgca agcctaacaa tatggttccc cttgtttcag  120
gccaatacac caccagcagt tctgcttgat cagctaaaga ctctgactat aactactctg  180
tatgctgcat cacaaagtgg tccaatacta aaagtgaatg catcagccca gggtgcagca  240
atgtctgtac ttcccaaaaa gtttgaagtc aatgcgactg tagcacttga cgaatatagc  300
aaattagaat ttgacaaact tacagtctgt gaagtaaaaa cagtttactt aacaaccatg  360
aaaccatatg ggatggtatc aaagtttgtg agctcggcca aatcagttgg caaaaaaaca  420
catgatctaa tcgcattatg tgatttttatg gatctagaaa agaacacacc agttacaata  480
ccagcattta tcaaatcagt ttctatcaag gagagtgaat cagccactgt tgaagctgca  540
```

```
ataagcagtg aagcagacca agctctaaca caagccaaaa ttgcacctta tgcgggactg 600
atcatgatta tgaccatgaa caatcccaaa ggcatattca agaagcttgg agctgggacc 660
caagttatag tagaactagg agcatatgtc caggctgaaa gcataagtaa aatatgcaag 720
acttggagcc atcaaggaac aagatatgtg ctgaagtcca gttaa             765
```

<210> 364
<211> 765
<212> DNA
<213> human metapneumo virus

<400> 364
```
atggagtcct atctagtaga cacttatcaa ggcattccat atacagctgc tgttcaagtt 60
gacctggtag aaaaagattt actgccagca agtttgacaa tatggtttcc tttatttcag 120
gccaacacac caccagcagt tctgcttgat cagctaaaaa ccttgacaat aacaactctg 180
tatgctgcat cacagaatgg tccaatactc aagtaaatg catctgccca aggtgctgcc 240
atgtctgtac ttcccaaaaa attcgaggta aatgcaactg tagcacttga tgaatacagt 300
aaacttgatt ttgacaagct gacggtctgc gatgttaaaa cagtttattt gacaaccatg 360
ccagcatica taaagtcagt tcaatcaaa agttcagcca aatcagttgg caaaaagaca 420
catgatctaa ttgcactatg tgacttcatg gacctagaga aaaatatacc tgtgacaata 480
ataagcagcg aagccgacca agctttgaca caagccaaga ttgcgcccta tgcaggacta 540
attatgatca tgaccatgaa caatccaaaa ggtatattca agaaactagg ggctggaaca 600
caagtgatag tagagctggg ggcatatgtt caggctgaga gcatcagtag gatctgcaag 720
agctggagtc accaaggaac aagatacgta ctaaaatcca gataa            765
```

<210> 365
<211> 765
<212> DNA
<213> human metapneumo virus

<400> 365
```
atggagtcct atctagtgga cacttatcaa ggcattccct acacagctgc tgttcaagtt 60
gatctggtag aaaaagactt actaccagca agtttgacaa tatggtttcc tctattccaa 120
gccaacacac caccagcagt tttgcttgat cagctaaaaa ccttgactat catcagtctca 180
tatgctgcat cacagaatgg tccaatactc aaagtaaatg catcagctca gggtgctgct 240
atgtctgtac ttcccaaaaa attcgaagta aatgcaactg tggcacttga tgaatacagc 300
aaacttgact ttgacaagct aacggtttgc gatgttaaaa cagtttattt gacaaccatg 360
aagccatatg ggatggtgtc aaaatttgtg agttcagcca aatcagttgg caaaaagaca 420
catgatctaa ttgcactgtg tgacttcatg gacctagaga aaaatatacc tgtgacaata 480
ccagcattca taaagtcagt ttcaatcaaa gagagtgagt cagccactgt tgaagctgca 540
ataagcagtg aggccgacca agctattaca caagccaaaa ttgcacccta tgcaggacta 600
atcatgatca tgaccatgaa caatccaaaa ggtatattca agaaactagg agctggaaca 660
caagtgatag tagagctagg ggcatatgtt caagccgaga gcatcagcag gatctgcaag 720
agctggagtc accaaggaac aagatatgta ctaaaatcca gataa            765
```

<210> 366
<211> 394
<212> PRT
<213> human metapneumo virus

<400> 366
```
Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
1               5                   10                  15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
            20                  25                  30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
        35                  40                  45
Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
    50                  55                  60
Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
65                  70                  75                  80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
```

```
                          85                        90                        95
     Thr Tyr Ser Leu Gly Lys Ile Lys Asn Asn Lys Gly Glu Asp Leu Gln
                     100                       105                       110
     Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
                115                       120                       125
     Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
          130                       135                       140
     Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
     145                       150                       155                       160
     Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
                          165                       170                       175
     Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
                     180                       185                       190
     Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
                195                       200                       205
     Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr His Arg Ser Leu Phe
          210                       215                       220
     Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
     225                       230                       235                       240
     Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
                          245                       250                       255
     Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
                     260                       265                       270
     Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
                275                       280                       285
     Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
          290                       295                       300
     Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
     305                       310                       315                       320
     Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
                          325                       330                       335
     Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
                     340                       345                       350
     Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
                355                       360                       365
     Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
          370                       375                       380
     Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
     385                       390


     <210> 367
     <211> 394
     <212> PRT
     <213> human metapneumo virus

     <400> 367
     Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
     1                   5                        10                       15
     Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
                20                       25                       30
     Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
          35                       40                       45
     Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
     50                       55                       60
     Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
     65                       70                       75                       80
     Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
                          85                       90                       95
     Thr Tyr Ser Leu Gly Lys Val Lys Asn Asn Lys Gly Glu Asp Leu Gln
                     100                       105                       110
     Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
```

```
              115                    120                      125
Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
    130                    135                    140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
145                    150                    155                    160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
                   165                    170                    175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
               180                    185                    190
Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
           195                    200                    205
Ser Phe Tyr Asp Leu Phe Gln Lys Val Tyr Tyr Arg Ser Leu Phe
       210                    215                    220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Thr Gly Ser Lys Ala
225                    230                    235                    240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
                   245                    250                    255
Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
           260                    265                    270
Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
       275                    280                    285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
   290                    295                    300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305                    310                    315                    320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
                   325                    330                    335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
           340                    345                    350
Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
       355                    360                    365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
   370                    375                    380
Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
385                    390
```

<210> 368
<211> 394
<212> PRT
<213> human metapneumo virus

<400> 368
```
Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
1                  5                      10                     15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
               20                     25                     30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
           35                     40                     45
Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu
       50                     55                     60
Ile Gly Ile Gln Tyr Ile Cys Thr Ala Leu Gly Ser Glu Arg Val Gln
65                     70                     75                     80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Lys
               85                     90                     95
Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
           100                    105                    110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Ile Glu Glu Ile Asp
       115                    120                    125
Lys Glu Ala Arg Lys Thr Met Val Thr Leu Leu Lys Glu Ser Ser Gly
    130                    135                    140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
```

180

```
145                    150                    155                    160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
                165                    170                    175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
            180                    185                    190
Asp Ala Leu Lys Arg Tyr Pro Arg Ile Asp Ile Pro Lys Ile Ala Arg
        195                    200                    205
Ser Phe Tyr Glu Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
    210                    215                    220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
225                    230                    235                    240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
                245                    250                    255
Thr Leu Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
            260                    265                    270
Leu Gly His Val Ser Val Gln Ser Glu Leu Lys Gln Val Thr Glu Val
        275                    280                    285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
    290                    295                    300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305                    310                    315                    320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
                325                    330                    335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
            340                    345                    350
Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
        355                    360                    365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
    370                    375                    380
Met Ser Gly Asp Asn Gln Asn Asp Tyr Glu
385                    390
```

```
<210> 369
<211> 394
<212> PRT
<213> human metapneumo virus

<400> 369
Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
1                      5                      10                     15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
                20                     25                     30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
        35                     40                     45
Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu
    50                     55                     60
Ile Gly Ile Gln Tyr Ile Cys Thr Ala Leu Gly Ser Glu Arg Val Gln
65                     70                     75                     80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Lys
                85                     90                     95
Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
        100                    105                    110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
    115                    120                    125
Lys Glu Ala Arg Lys Thr Met Val Thr Leu Leu Lys Glu Ser Ser Gly
130                    135                    140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
145                    150                    155                    160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
                165                    170                    175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
```

```
                180                    185                    190
Asp Ala Leu Lys Arg Tyr Pro Arg Val Asp Ile Pro Lys Ile Ala Arg
            195                    200                    205
Ser Phe Tyr Glu Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
    210                    215                    220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
225                    230                    235                    240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
                245                    250                    255
Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
            260                    265                    270
Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
        275                    280                    285
Tyr Asp Leu Val Arg Glu Met Glu Pro Glu Ser Gly Leu Leu His Leu
    290                    295                    300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305                    310                    315                    320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
                325                    330                    335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
            340                    345                    350
Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
        355                    360                    365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
    370                    375                    380
Met Ser Asp Asp Asn Gln Asp Asp Tyr Glu
385                    390
```

```
<210> 370
<211> 1185
<212> DNA
<213> human metapneumo virus

<400> 370
atgtctcttc aagggattca cctgagtgat ttatcataca agcatgctat attaaaagag  60
tctcagtaca caataaaaag agatgtgggt acaacaactg cagtgacacc ctcatcattg  120
caacaagaaa taacactgtt gtgtggagaa attctgtatg ctaaacatgc tgactacaaa  180
tatgctgcag aaataggaat acaatatatt agcacagctt taggatcaga gagagtgcag  240
cagattctga ggaactcagg cagtgaagtc caagtggtct taaccagaac gtactctctg  300
gggaaaatta aaacaataa aggagaagat ttacagatgt tagacataca cgggtagag  360
aagagctggg tagaagagat agacaaagaa gcaatggaaa caatggcaac cttgcttaag  420
gaatcatcag gtaatatccc acaaaatcag aggccctcag caccagacac acccataatc  480
ttattatgtg taggtgcctt aatattcact aaactagcat caaccataga agtgggacta  540
gagaccacag tcagaagggc taacgtgta ctaagtgatg cactcaagag atacctaga  600
atggacatac caaagattgc cagatcctc tatgacttat ttgaacaaa agtgtatcac  660
agaagtttgt tcattgagta tggcaaagca ttagctcat catctacagg cagcaaagca  720
gaaagtctat ttgttaatat attcatgcaa gcttatgggg ccggtcaaac aatgctaagg  780
tggggtca ttgccaggtc atccaacaat ataatgttag gacatgtatc cgtccaagct  840
gagttaaaac aggtcacaga agtctatgac ttggtgcgag aaatgggccc tgaatctgga  900
cttctacatt taaggcaaag cccaaaagct ggactgttat cactagccaa ctgtcccaac  960
tttgcaagtg ttgttctcgg aaatgcctca ggcttaggca taatcggtat gtatcgaggg 1020
agagtaccaa acacagaatt attttcagca gctgaaagtt atgccaaaag tttgaaagaa 1080
agcaataaaa taaatttctc ttcattagga cttacagatg aagagaaaga ggctgcagaa 1140
catttcttaa atgtgagtga cgacagtcaa aatgattatg agtaa                  1185

<210> 371
<211> 1185
<212> DNA
<213> human metapneumo virus

<400> 371
```

```
atgtctcttc aagggattca cctgagtgat ctatcataca agcatgctat attaaaagag   60
tctcagtata caataaaagg agatgtaggc acaacaaccg cagtgacacc ctcatcattg  120
caacaagaaa taacactatt gtgtggagaa attctatatg ctaagcatgc tgattacaaa  180
tatgctgcag aaatagggat acaatatatt agcacagctc taggatcaga gagagtacag  240
cagattctaa gaaactcagg tagtgaagtc caagtggttt taaccagaac gtactccttg  300
gggaaagtta aaaacaacaa aggagaagat ttacagtgtt tagacataca cggaagtggaa  360
aaaagctggg tggaagagat agacaagaga gcaagaaaaa caatggcaac tttgcttaaa  420
gaatcatcag gcaatatcac acaaaatcag aggccttcag caccagacac accaataatt  480
ttattatgtg taggtgcctt aatattacc aaactagcat caactataga agtgggatta  540
gagaccacag tcagaagagc taaccgtgta ctaagtgatg cactcaaaag atacccaagg  600
atggacatac caaaaatcgc tagatctttc tatgacttat ttgaacaaaa agtgtattac  660
agaagtttgt tcattgagta tggcaaagca ttaggctcat cctctacagg cagcaaagca  720
gaaagtttat tcgttaatat attcatgcaa gcttacggtg ctggtcaaac aatgctgagg  780
tggggagtca ttgccaggtc atctaacaat ataatgttgg gacatgtatc tgttcaagct  840
gagttaaaac aagtcacaga agtctatgac ctggtgcgag aaatgggccc tgaatctggg  900
ctcctacatt taaggcaaag cccaaaagct ggactgttat cactagccaa ttgtcccaac  960
tttgctagtg ttgttctcgg caatgcctca ggctaggca taataggtat gtatcgcggg 1020
agagtgccaa acacagaact attttcagca gcagaagtt atgccaagag tttgaaagaa 1080
agcaataaaa ttaactttc ttcattagga ctcacacatg aagaaaaga ggctgcagaa 1140
cacttcctaa atgtgagtga cgacagtcaa aatgattatg agtaa               1185
```

<210> 372
<211> 1185
<212> DNA
<213> human metapneumo virus

<400> 372
```
atgtctcttc aagggattca cctaagtgat ctatcatata aacatgctat attaaaagag   60
tctcaataca caataaaaag agatgtaggc acaacaactg cagtgacacc ttcatcatta  120
caacaagaaa taacactttt gtgtgggaa atactttaca ctaaacacac tgattacaaa  180
tatgctgcag agatagggat acaatatatt tgcacagctc taggatcaga aagagtacaa  240
cagatttttga gaaactcagg tagtgaagtt caggtggttc taaccaaaac atactcctta  300
aagagttgga tagaagaaat agacaagaga gcaagaaaga caatggtaac tttgcttaag  360
gaatcatcag gtaacatccc acaaaaccag agacttcag caccagacac accaataatt  420
ttattatgtg taggtgccct aatattcact aaactagcat caacaatag agttggatta  480
gagactacag ttagaagagc taataagtg ctaagtgat cactcaaaag atacccaagg  540
agaagtttat tcattgagta cggaaaagct ttaggctcat cttcaacagg aagcaaagca  600
gaaagtttat ttgtaaatat atttatgcaa gcttatggag ctggtcaaac acttatgagg  720
tggggtgtca ttgccagatc atccaacaac ataatgctag ggcatgtatc tgtgcaatct  840
gaattgaagc aagtcacaga ggttatgac ttggtgagag aatgggtcc tgaatctggg  900
ctttacatc taagacaaag tccaaagca gggctgttat cattggccaa ttgccccaat  960
tttgctagtg ttgttcttgg caatgcctca gtctaggcca taatcggaat gtacagaggg 1020
agagtaccaa acacagagct attttctgca gcagaaagtt atgccagaag cttaaaagaa 1080
agcaataaaa tcaacttctc ttcgttaggg cttacagatg aagaaaaaga agctgcagaa 1140
cacttcttaa acatgagtgg tgacaatcaa aatgattatg agtaa               1185
```

<210> 373
<211> 1185
<212> DNA
<213> human metapneumo virus

<400> 373
```
atgtctcttc aagggattca cctaagtgat ctgtcatata aacatgctat attaaaagag   60
tctcaataca caataaaaag agatgtaggc accacaactg cagtgacacc ttcatcattg  120
cagcaagaaa taacacttt gtgtggagag attctttaca ctaaacatac tgattacaaa  180
tatgctgcag agatagggat acaatatatt tgcacagctc taggatcaga aagagtacaa  240
cagattttaa gaaactcagg tagtgaagtt caggtggttc taaccaagac atactcctta  300
gggaaaggta aaaatagtaa agggaaagat ttgcaaatgt tagatataca tggagtggaa  360
aagagttggg tagaagaaat agacaagaga gcaagaaaag caatggtaac tttgctaaag  420
gaatcatcag gcaacatccc acaaaaccag aggccttcag caccagacac accaataatt  480
```

```
ttattgtgtg taggtgcttt aatattcact aaactagcat caacaatagaa agttggacta 540
gagactacag ttagaagggc taacagagtg ttaagtgatg cgctcaaaag atacccctagg 600
gtagatatac caaagattgc tagatctttt tatgaactat ttgagcagaa agtgtattac 660
aggagtctat tcattggagta tgggaaagct ttaggctcat cttcaacagg aagcaaagca 720
gaaagtttgt ttgtaaatat atttatgcaa gcttatggag ccggtcagac aatgctaagg 780
tggggtgtca ttgccagatc atctaacaac ataatgctag ggcatgtatc tgtgcaagct 840
gaatcgaaac aagttacaga agtttatgat ttggtaagag aaatgggtcc tgaatctggg 900
ctttacatc taagacaaag tccaaaggca ggactgttat cgttggctaa ttgccccaat 960
tttgctgagtg ttgttcttgg taatgcttca ggtctaggta taatcggaat gtacaggggga 1020
agagtgccaa acacagagct attttctgca gcagaaagtt atgccagaag cttaaaagaa 1080
agcaacaaaa tcaacttctc ctcattaggg ctcacagacg aagaaaaaga agctgcagaa 1140
cacttcttaa acatgagtga tgacaatcaa gatgattatg agtaa 1185
```

<210> 374
<211> 294
<212> PRT
<213> human metapneumo virus

<400> 374

```
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
1               5                   10                  15
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Gly His
            20                  25                  30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu
        35                  40                  45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Ala Lys Pro Thr Ile Pro
    50                  55                  60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Thr Lys Thr
65                  70                  75                  80
Glu Ile Lys Gln Ala Ile Lys Val Met Asp Pro Ile Glu Glu Glu Glu
                85                  90                  95
Ser Thr Glu Lys Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
            100                 105                 110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Lys Val Ser Phe
        115                 120                 125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
    130                 135                 140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145                 150                 155                 160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Ala Leu
                165                 170                 175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
            180                 185                 190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
        195                 200                 205
Asp Ala Met Ile Gly Val Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys
    210                 215                 220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Ser Gln
225                 230                 235                 240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
                245                 250                 255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
            260                 265                 270
Glu Glu Glu Glu Pro Lys Asp Thr Gln Asp Asn Ser Gln Glu Asp Asp
        275                 280                 285
Ile Tyr Gln Leu Ile Met
        290
```

<210> 375
<211> 294
<212> PRT

184

<213> human metapneumo virus

<400> 375
```
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
1               5                   10                  15
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Asn His
            20                  25                  30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu
        35                  40                  45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Thr Lys Pro Thr Ile Leu
    50                  55                  60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Ile Lys Thr
65                  70                  75                  80
Glu Ala Lys Gln Thr Ile Lys Val Met Asp Pro Ile Glu Glu Glu Glu
            85                  90                  95
Phe Thr Glu Lys Arg Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
            100                 105                 110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Lys Val Ser Phe
        115                 120                 125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
    130                 135                 140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145                 150                 155                 160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
            165                 170                 175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
        180                 185                 190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
        195                 200                 205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys
210                 215                 220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln
225                 230                 235                 240
Arg Thr Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
            245                 250                 255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
        260                 265                 270
Glu Glu Glu Glu Pro Lys Asp Thr Gln Glu Asn Asn Gln Glu Asp Asp
        275                 280                 285
Ile Tyr Gln Leu Ile Met
    290
```

<210> 376
<211> 294
<212> PRT
<213> human metapneumo virus

<400> 376
```
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
1               5                   10                  15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Lys Ser Gly His
            20                  25                  30
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu
        35                  40                  45
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu
    50                  55                  60
Leu Glu Pro Lys Leu Ala Trp Ala Asp Asn Ser Gly Ile Thr Lys Ile
65                  70                  75                  80
Thr Glu Lys Pro Ala Thr Lys Thr Thr Asp Pro Val Glu Glu Glu Glu
            85                  90                  95
Phe Asn Glu Lys Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
```

```
                100                    105                    110
Glu Lys Lys Ser Lys Phe Ser Thr Ser Val Lys Lys Lys Val Ser Phe
                    115                    120                    125
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
            130                    135                    140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145                    150                    155                    160
Thr Phe Glu Glu Lys Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
                    165                    170                    175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
                180                    185                    190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
                195                    200                    205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys
            210                    215                    220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln
225                    230                    235                    240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
                    245                    250                    255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
            260                    265                    270
Glu Glu Glu Glu Pro Lys Glu Thr Gln Asp Asn Asn Gln Gly Glu Asp
        275                    280                    285
Ile Tyr Gln Leu Ile Met
        290


<210> 377
<211> 294
<212> PRT
<213> human metapneumo virus

<400> 377
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
1               5                   10                  15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Arg Ser Gly His
                20                  25                  30
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu
        35                  40                  45
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu
    50                  55                  60
Leu Glu Pro Lys Leu Ala Trp Ala Asp Ser Ser Gly Ala Thr Lys Thr
65                  70                  75                  80
Thr Glu Lys Gln Thr Thr Lys Thr Thr Asp Pro Val Glu Glu Glu Glu
                85                  90                  95
Leu Asn Glu Lys Lys Val Ser Pro Ser Ser Asp Gly Lys Thr Pro Ala
                100                    105                    110
Glu Lys Lys Ser Lys Ser Pro Thr Asn Val Lys Lys Lys Val Ser Phe
                115                    120                    125
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
            130                    135                    140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145                    150                    155                    160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
                    165                    170                    175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
                180                    185                    190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
                195                    200                    205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys
            210                    215                    220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln
```

```
225                   230                   235                   240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
                         245                   250                   255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
                   260                   265                   270
Glu Glu Glu Glu Pro Lys Glu Thr Gln Asp Asn Asn Gln Gly Glu Asp
          275                   280                   285
Ile Tyr Gln Leu Ile Met
          290
```

<210> 378
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 378
```
atgtcattcc ctgaaggaaa agatattctt ttcatgggta atgaagcagc aaaattagca    60
gaagctttcc agaaatcatt aagaaaacca ggtcataaaa gatctcaatc tattatagga   120
gaaaaagtga atactgtatc agaaacattg gaattaccta ctatcagtag acctgcaaaa   180
ccaaccatac cgtcagaacc aaagttagca tggacagata aaggtggggc aaccaaaact   240
gaaataaagc aagcaatcaa agtcatggat cccattgaag aagaagagtc taccgagaag   300
aaggtgctac cctccagtga tgggaaaacc cctgcagaaa agaaactgaa accatcaact   360
aacaccaaaa agaaggtttc atttacacca aatgaaccag ggaaatatac aaagttggaa   420
aaagatgctc tagatttgct ctcagataat gaagaagaag atgcagaatc ttcaatctta   480
acctttgaag aaagagatac ttcatcatta agcattgagg ccagattgga atcaatagag   540
gagaaattaa gcatgatatt agggctatta agaacactca acattgctac agcaggaccc   600
acagcagcaa gagatgggat cagagatgca atgattggcg taagagagga attaatagca   660
gacataataa aggaagctaa agggaaagca gcagaaatga tggaagagaa aatgagtcaa   720
cgatcaaaaa taggaaatgg tagtgtaaaa ttaacagaaa aagcaaaaga gctcaacaaa   780
attgttgaag atgaaagcac aagtggagaa tccgaagaag aagaagaacc aaaagacaca   840
caagacaata gtcaagaaga tgacatttac cagttaatta tgtag               885
```

<210> 379
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 379
```
atgtcattcc ctgaaggaaa agatattctt ttcatgggta atgaagcagc aaaattggca    60
gaagcttttc aaaaatcatt aagaaaacct aatcataaaa gatctcaatc tattatagga   120
gaaaaagtga acactgtatc tgaaacattg gaattaccta ctatcagtag acctgcaaaa   180
ccgaccatat tgtcagagcc gaagttagca tggacagaca aaggtggggc aatcaaaact   240
gaagcaaagc aaacaatcaa agttatggat cctattgaag aagaagagtt tactgagaaa   300
agggtgctgc cctccagtga tgggaaaacc cctgcagaaa agaagttgaa accatcaacc   360
aacactaaaa agaaggtctc atttacacca aatgaaccag gaaaatacac aaagttggag   420
aaagatgctc tagacttgct ttcagacaat gaagaagaag atgcagaatc ctcaatctta   480
acctctgaag aaagagatac ttcatcatta agcattgaag ccagactaga atcgattgag   540
gagaaattaa gcatgatatt agggctatta agaacactca acattgctac agcaggaccc   600
acagcagcaa gagatgggat cagagatgca atgattggca taagggagga actaatagca   660
gacataataa aagaagccaa gggaaaagca gcagaaatga tggaagagaa aatgaaccag   720
cggacaaaaa taggaaacgg tagtgtaaaa ttaactgaaa aggcaaagga gctcaacaaa   780
attgttgaag acgaaagcac aagtggtgaa tccgaagaag aagaagaacc aaaagacaca   840
caggaaaata atcaagaaga tgacatttac cagttaatta tgtag               885
```

<210> 380
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 380
```
atgtcattcc ctgaaggaaa ggatattctg ttcatgggta atgaagcagc aaaaatagcc    60
```

187

```
gaagctttcc agaaatcact gaaaaaatca ggtcacaaga gaactcaatc tattgtaggg 120
gaaaaagtta acactatatc agaaacctca gaactaccta ccatcagcaa acctgcacga 180
tcatctacac tgctggaacc aaaattggca tgggcagaca acagcggaat caccaaaatc 240
acagaaaaac cagcaaccaa aacaacagat cctgttgaag aagaggaatt caatgaaaag 300
aaagcgttac cttccagtga tgggaagact cctgcagaga aaaatcaaa gttttcaacc 360
agtgtaaaaa agaaagtttc cttcacatca aatgaaccag ggaaatacac caaactagag 420
aaagatgccc tagatttgct ctcagacaat gaggaagaag acgcagaatc ctcaatccta 480
acttttgagg agaaagatac atcatcacta agcattgaag ctagactaga atctatagaa 540
gagaagttga gcatgatatt aggactgctt cgtacactta acattgcaac agcaggacca 600
acagctgcac gagatggaat tagggatgca atgattggta taagagaaga gctaatagca 660
gagataatta aggaagccaa gggaaaagca gctgaaatga tggaagaaga gatgaatcaa 720
agatcaaaaa taggtaaatg cagtgtaaaa ctaaccgaga aggcaaaaga gctcaacaaa 780
attgttgaag acgagagcac aagcggtgaa tcagaagaag aagaagaacc aaaagaaact 840
caggataaca atcaaggaga agatatttat cagttaatca tgtag            885
```

```
<210> 381
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 381
atgtcattcc ctgaaggaaa agatatcctg ttcatggta atgaagcagc aaaaatagca 60
gaagctttcc agaaatcact aaaaagatca ggtcacaaaa gaacccagtc tattgtaggg 120
gaaaaagtaa acactatatc agaaactcta gagctaccta ccatcagcaa acctgcacga 180
tcatctacac tgctagagcc aaaattggca tgggcagaca gcagcggagc caccaaaatc 240
acagaaaaac aaacaaccaa aacaacagat cctgttgaag aagaggaact caatgaaaag 300
aagtatcac cttccagtga tgggaagact cctgcagaga aaaatcaaa atctccaacc 360
aatgtaaaaa agaaagtttc cttcacatca aatgaaccag ggaaatatac taaactagaa 420
aaagatgccc tagatttgct ctcagacaat gaggaagaag acgcagagtc ctcaatccta 480
acttttgaag agagagacac atcatcacta agcattgagg tagactaga atcaatagaa 540
gagaagctaa gcatgatatt aggactgctt cgtacactta acattgcaac agcaggacca 600
acggctgcaa gggatggaat cagagatgca atgattggta taagagaaga actaatagca 660
gaaataataa aagaagcaaa gggaaaagca gccgaaatga tggaagaaga aatgaatcaa 720
aggtcaaaaa taggtaatgg cagtgtaaaa ctaaccgaga aggcaaaaga acttaataaa 780
attgttgaag acgagagcac aagtggtgaa tcagaagaag aagaagaacc aaaagaaact 840
caggataaca atcaaggaga agatatctac cagttaatca tgtag            885
```

```
<210> 382
<211> 183
<212> PRT
<213> human metapneumo virus

<400> 382
```

Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys
1 5 10 15

```
Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys
1               5                   10                  15
Thr His Leu Lys Lys Ile Ile Lys Asp His Ser Gly Lys Val Leu Ile
            20                  25                  30
Val Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Leu Thr Val Thr Ile
        35                  40                  45
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser
    50                  55                  60
Lys Thr Glu Ser Asp Lys Lys Asp Ser Ser Ser Asn Thr Thr Ser Val
65                  70                  75                  80
Thr Thr Lys Thr Thr Leu Asn His Asp Ile Thr Gln Tyr Phe Lys Ser
                85                  90                  95
Leu Ile Gln Arg Tyr Thr Asn Ser Ala Ile Asn Ser Asp Thr Cys Trp
            100                 105                 110
Lys Ile Asn Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu
        115                 120                 125
Cys Phe Lys Ser Glu Asp Thr Lys Thr Asn Asn Cys Asp Lys Leu Thr
    130                 135                 140
Asp Leu Cys Arg Asn Lys Pro Lys Pro Ala Val Gly Val Tyr His Ile
```

```
145                    150                    155                    160
Val Glu Cys His Cys Ile Tyr Thr Val Lys Trp Lys Cys Tyr His Tyr
                    165                    170                    175
Pro Thr Asp Glu Thr Gln Ser
                    180


<210> 383
<211> 179
<212> PRT
<213> human metapneumo virus

<400> 383
Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys
1                    5                     10                    15
Thr His Leu Lys Lys Ile Ile Lys Asp His Ser Gly Lys Val Leu Ile
                    20                    25                    30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ile Thr Ile
                    35                    40                    45
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser
            50                    55                    60
Lys Thr Glu Ser Asp Lys Glu Asp Ser Pro Ser Asn Thr Thr Ser Val
65                    70                    75                    80
Thr Thr Lys Thr Thr Leu Asp His Asp Ile Thr Gln Tyr Phe Lys Arg
                    85                    90                    95
Leu Ile Gln Arg Tyr Thr Asp Ser Val Ile Asn Lys Asp Thr Cys Trp
            100                    105                    110
Lys Ile Ser Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu
            115                    120                    125
Cys Phe Lys Pro Glu Asp Ser Lys Ile Asn Ser Cys Asp Arg Leu Thr
            130                    135                    140
Asp Leu Cys Arg Asn Lys Ser Lys Ser Ala Ala Glu Ala Tyr His His
145                    150                    155                    160
Val Glu Cys His Cys Ile Tyr Thr Ile Glu Trp Lys Cys Tyr His His
                    165                    170                    175
Pro Ile Asp


<210> 384
<211> 177
<212> PRT
<213> human metapneumo virus

<400> 384
Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys
1                    5                     10                    15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Val Leu Ile
                    20                    25                    30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ala Thr Ile
            35                    40                    45
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Pro
            50                    55                    60
Lys Asn Glu Ser Asp Lys Lys Val Thr Lys Pro Asn Thr Thr Ser Thr
65                    70                    75                    80
Thr Ile Arg Pro Thr Pro Asp Pro Thr Val Val His His Leu Lys Arg
                    85                    90                    95
Leu Ile Gln Arg His Thr Asn Ser Val Thr Lys Asp Ser Asp Thr Cys
            100                    105                    110
Trp Arg Ile His Lys Asn Gln Cys Thr Asn Ile Lys Ile Tyr Lys Phe
            115                    120                    125
Leu Cys Ser Gly Phe Thr Asn Ser Lys Gly Thr Asp Cys Glu Glu Pro
```

```
         130                      135                  140
Thr Ala Leu Cys Asp Lys Lys Leu Lys Thr Ile Val Glu Lys His Arg
145                      150                  155                  160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Gly Cys Leu His
                 165                  170                  175
Pro
```

```
<210> 385
<211> 177
<212> PRT
<213> human metapneumo virus

<400> 385
Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys
1                   5                  10                  15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Leu Leu Ile
                 20                  25                  30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Val Thr Ile
         35                  40                  45
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Leu
      50                  55                  60
Lys Asn Glu Ser Asp Lys Lys Asp Thr Lys Leu Asn Thr Thr Ser Thr
65                   70                  75                  80
Thr Ile Arg Pro Ile Pro Asp Leu Asn Ala Val Gln Tyr Leu Lys Arg
                 85                  90                  95
Leu Ile Gln Lys His Thr Asn Phe Val Ile Lys Asp Arg Asp Thr Cys
                 100                 105                 110
Trp Arg Ile His Thr Asn Gln Cys Thr Asn Ile Lys Ile Tyr Lys Phe
         115                 120                 125
Leu Cys Phe Gly Phe Met Asn Ser Thr Asn Thr Asp Cys Glu Glu Leu
         130                 135                 140
Thr Val Leu Cys Asp Lys Lys Ser Lys Thr Met Thr Glu Lys His Arg
145                 150                 155                 160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Trp Cys Tyr Tyr
                 165                 170                 175
Leu
```

```
<210> 386
<211> 552
<212> DNA
<213> human metapneumo virus

<400> 386
atgataacct tagatgtcat taaaagtgat gggtcttcaa aaacatgtac tcacctcaaa  60
aaaataatta aagaccactc tggtaaagtg cttattgtac ttaagttaat attagcttta 120
ctaacatttc tcacagtaac aatcaccatc aattatataa aagtggaaaa caatctgcaa 180
atatgccagt caaaaactga atcagacaaa aaggactcat catcaaatac cacatcagtc 240
acaaccaaga ctactctaaa tcatgatatc acacagtatt ttaaaagttt gattcaaagg 300
tatacaaact ctgcaataaa cagtgacaca tgctggaaaa taaacagaaa tcaatgcaca 360
aatataacaa catacaaatt tttatgtttt aaatctgaag acacaaaaac caacaattgt 420
gataaactga cagatttatg cagaaacaaa ccaaaaccag cagttggagt gtatcacata 480
gtagaatgcc attgtatata cacagttaaa tggaagtgct atcattaccc aaccgatgaa 540
acccaatcct aa                                                      552
```

```
<210> 387
<211> 540
<212> DNA
<213> human metapneumo virus
```

190

```
<400> 387
atgataacat tagatgtcat taaaagtgat gggtcttcaa aaacatgtac tcacctcaaa 60
aaaataatca aagaccattc tggtaaagtg cttattgcac ttaagttaat attagcttta 120
ctaacatttt tcacaataac aatcactata aattacataa aagtagaaaa caattctacaa 180
atatgccagt ccaaaactga atcagacaaa gaagactcac catcaaatac cacatccgtc 240
acaaccagca ctactctaga ccatgatata acacagtatt ttaaaagatt aattcaaagg 300
tatacagatt ctgtgataaa caaggacaca tgctcgaaaa taagcagaaa tcaatgcaca 360
aatataacaa catataaatt tttatgcttt aaacctgagg actcaaaaat caacagttgt 420
gatagactga cagatctatg cagaaacaaa tcaaaatcag cagctgaagc atatcataca 480
gtagaatgcc attgcatata cacaattgag tggaagtgct atcaccaccc aatagattaa 540


<210> 388
<211> 534
<212> DNA
<213> human metapneumo virus

<400> 388
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<213> human metapneumo virus

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